

From:

Mertz, Prema

Sent:

Wednesday, August 16, 2000 9:07 AM

To:

STIC-Biotech/ChemLib

Subject:

09/361,655

Please search SEQ ID NO: with protein databases.

Thanks

Prema Med;

Prema Mertz, Ph.D. Primary Examiner

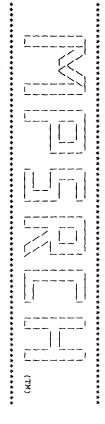
Crystal Mall 1, Room 10E01

Art Unit 1646 (703)308-4229

U.S. Patent & Trademark Office

Edward Hart Technical Info Specialist STIC / Biotech CMI 12C14 Tel: 305-9203

CAG 12C1 IN TO STEELS



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Run on: rch_pp protein - protein database search, using Smith-Waterman algorithm Thu Aug 17 10:15:21 2000; MasPar time 5.52 Seconds 510.994 Million cell updates/sec

Description: Perfect Score: Tabular output not generated. >US-08-765-662-12 (1-119) from 5929213.pep 916

Sequence: 1 RARRETPICEPAIPLCCRRD......NGNVVKTDVPDMVVEACGCS 119

Scoring table: PAM 150 Gap 11

188963 seqs, 23686106 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq36 1:geneseqp

Statistics: Mean 29.911; Variance 113.258; scale 0.264

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length DB	Ħ	Description	Pred. No.
1	916	100.0		R92754	Human growth different	1.15e-87
2	913		350 1	W60619	liver a	2.48e-87
w	906	98.9		W60618	Murine liver activin b	1.49e-86
4	632			W60617	Murine liver activin b	3.36e-56
U	616	7.		R89729	prming	1.93e-54
σ	608			R10991		1.46e-53
7	498	54.4		P60520	e of h	1.54e-41
8	498	54.4		P60518	Sequence of bovine inh	1.54e-41
9	498	54.4	426 1	P70203	Sequence of human inhi	1.54e-41
10	498	54.4		R05413	BUF-3 human differenti	1.54e-41
11	498	54.4		P70200	Sequence of porcine in	1.54e-41
12	486	53.1		R10990	30ne	3.09e-40
13	477			R12088		2.93e-39
14	476	52.0		R26481	Activin-like peptide.	w
15	472			P80019	Sequence of the 14K be	1.02e-38
16	472			R05443	Monomer A of BUF-4.	1.02e-38
17	472	٠		P82061	Polypeptide BUF-3 for	1.02e-38
18	472			P71176	Second protein chain o	1.02e-38
19	472			R25128	Activin AB.	1.02e-38
20	472			R31622	BUF~3.	1.02e-38
21	472	51.5		R08215	Follicle stimulating h	1.02e-38
22	472	٠	116 1	P71196	Sequence of vertebrate	1.02e-38
23	470	51.3		P70201	Sequence of porcine in	1.68e-38

γQ В

45	44	3	42	41	40	ي 9	3 8	37	36	u G	34	ယ္ထ	32	31	30	29	28	27	26	25	24
355	355	356	356	356	356	356	356	372	383	434	443	445	445	445	445	445	445	446	449	458	468
38.8	38.8	38.9	38.9	38.9	38.9	38.9	38.9	40.6	41.8	47.4	48.4	48.6	48.6	48.6	48.6	48.6	48.6	48.7	49.0	50.0	
398	119	172	172	172	172	172	115	101	101	116	115	116	115	115	115	115	115	87	115	116	505
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R10995	R10992	R51659	R85769	W89686	W44309	R44753	P91253	R89132	R89133	R05444	P80020	R25127	R31623	R25129	P71177	P71197	R08216	R45447	R26482	P81906	P10204
	Xenopus Bone Morphogen	Osteogenic fusion prot	CBMP2B1 fusion protein	Osteogenic fusion prot	Human osteogenic fusio	Osteogenic fusion prot	Protein COP-16.	Japanese carp beta-B a	Zebrafish beta-B activ	Monomer B of BUF-4 and	Sequence of the 14K be	Activin B.	BUF-4.	Human KHM-5M.	Second protein chain o	Sequence of vertebrate	Follicle stimulating h	TGF-beta-like clone MP	Activin-like peptide.	N-terminal of inhibin	sequence of numan inni
3.83e-20	3.83e-26	3.00e-26	3.00e-26	3.00e-26	3.00e-26	3.00e-26	3.00e-26	5.92e-28	3.95e-29	1.31e-34	1.40e-35	8.53e-36	8.53e-36	8.53e-36	8.53e-36	Ġ	8.53e-36	6.65e-36	3.15e-36	3.35e-37	:

ALIGNMENTS

% & O	So	6	200	S	8	38	38	S	ΡŢ	PT.	3 5	מ ק	Ţ	PA	PR	PR	Ä	8	Ž	1, 1, 1, 1,	H	Ŧ	Ϋ́	ΕŢ	Y	S	X	X	J (3 6	5	RESULT
Query Match 100.0%; Score 916; DB 1; Length 350; Best Local Similarity 100.0%; Pred. No. 1.15e-87; Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	liver cells in culture and to raise diagnostic antibodies. Sequence 350 AA;	such as hepatocellular carcinoma. In can also be used to expand	in the treatment of liver disorders, e.g. disease states in which liver function is compromised, or cellular proliferative disorders	host cells. GDF-12 possesses activities that will make it useful	of a cDNA clone (T16883) derived from adult liver in transformed	expressed specifically in liver. It can be obtd. by expression	Human growth differentiation factor-12 (GDF-12 - R92/54) is a new			and therapeutic methods esp, in methods for treating a cell	-	N-100000/11.	Esquela AF, Lee S;	<	26-SEP-1994; US-311370.	US-274	12-JUL-1995; U08745.	01-FEB-1996.		/label= C-terminal_region /note= "GFR-12 active C-terminal fragment"	. .	cleavage_site 232236		modified_site 198200	Key Location/Qualifiers	Homo sapiens.	factor	Growth differentiation factor-12; GDF-12; liver; cell proliferation;	Ginat Gillion Carlotter Control Carlotter Control Carlotter Carlot	21-,TIII-1996 (first entry)	R92/54 Standard; Protein; 350 AA.	

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                                                                                                                                                                                                                                                                                                     New isolated nucleic acid encoding sub-units of liver activin - In the stock of regulating growth and differentiation of cells, e.g. for treating liver, bone and haematopoietic disorders

Por treating liver, bone and haematopoietic disorders

Por bisclosure; Fig 5; 141pp; English.

Con this represents a human liver activin beta e polypeptide. The invention provides murine beta c and beta e polypeptides and the encoding genes.

Con bisorders of cell growth or differentiation (or susceptibility to them) are dispensed by measuring liver activin gene activity or by detecting a contact of the liver activin gene. Disorders of haematopoiesis, are dispensed by measuring liver activin gene activity or by detecting a contact of the liver activin gene conditions that can be secretion or cardiac morphogenesis are some conditions that can be compound or cardiac morphogenesis are some conditions that can be considered by treatment with an liver activin compound or agent that the compound suppregulates the compound's expression. Antagonists can be used to treat liver diseases while agonists can be used to increase growth and repensation of liver tissue. The liver activin compound may also induce the organization of liver tissue. The liver activin compound may also induce the mematopoiesis, particularly erythropolesis, for treating haemophilia, confidency in the processed and modified forms) proteins, or the transgenic containing liver activin gene can be used to produce the liver activin confidency in the confidency of the transgenic animals, are useful for screening for liver activin modulators.
                                                                                                                                                                                                                                            Query Match
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20-NOV-1997; U20882.
20-NOV-1996; US-752919.
(UNMI ) UNIV MICHICAN.
Bonadio J, Fang J;
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Liver activin; beta c; beta e; cell differentiation; haematopolesis;
erythroid; ovarian follicular maturation; hormone; neuronal survival;
spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis;
osteomalacia; erythropolesis; haemophilia; cystic fibrosis; immunoassay;
menstrual disorder; transgenic; modulator; human.
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                                                                                                                                                                                                                                                                                             sequence
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                             292 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 350
                                                                                                                          232 RARRRTFTCEPATFLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPFHLAGGPGIA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; V38240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domo sapiens.
61 ASFHSAVESLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 350
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                                                                                               1 RARRETPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 60
                                                                                                                                                                                                                      ocal
                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                             350 AA;
                                                                                                                                                                                              Conservative
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237. .3
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                                                                                                                                                                                                                      99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "mature growth factor domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Asn is putatively N-glycosylated"
                                                                                                                                                                                                                      Score 913; DB 1;
Pred. No. 2.48e-87;
                                                                                                                                                                                              Mismatches
                                                                                                                                                                                              0;
                                                                                                                                                                                                                                         Length 350;
                                                                                                                                                                                              Indels
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CC This represents a murine liver activin beta e polypeptide. Sequences CC derived from a beta c cDNA clone is used for screening and cloning the CC activin beta e gene. Disorders of cell growth or differentiation (or CC susceptibility to them) are diagnosed by measuring liver activin gene activity or by detecting a mutation in the liver activin gene. Disorders of cell growth or differentiation (or CC maturation, hormone secretion, neuronal survival, spermatogenesis, bone CC formation, insulin secretion or cardiac morphogenesis are some conditions that can be diagnosed using the liver activin. Cell growth and CC differentiation can be stimulated by treatment with an liver activin CC compound or agent that upregulates the compound's expression. Antagonists CC can be used to treat liver diseases while agonists can be used to CC increase growth and regeneration of liver tissue. The liver activin CC compound may also induce bone growth (e.g. for treating osteoporosis or CC treating haemophilia, cystic fibrosis or menstrual disorders. Antibodies (which the consecution of liver activin processed and modified forms) proteins, or transgenic animals containing liver activin gene can be used to produce the liver activin (in correctly processed and modified forms) proteins, compound containing are useful for screening for liver activin.
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Murine liver activin beta e polypeptide.
Liver activin; beta c; beta e; cell differentiation; haematopoiesis;
erythroid; ovarian follicular maturation; hormone; neuronal survival;
spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis;
spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis;
osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunoassay;
                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid encoding sub-units of liver activin - useful for regulating growth and differentiation of cells, e.g. for treating liver, bone and haematopoietic disorders (Claim 16, Fig 2; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W60618 standard; Protein; 350 AA. W60618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bonadio J, Fang J;
WPI; 98-312408/27.
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                                      232 RARRRTPTCEPETPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 291
                                                                                                                                                                   Local
1 RARRETPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 60
                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                       350 AA;
                                                                                                                                 Conservative
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237. .:
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22. .2:
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                                                                                                                                                            98.98;
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== "endoproteolytic cleavage site"
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.200
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                                                                                                                          Score 906; DB 1;
Pred. No. 1.49e-86;
2; Mismatches 1
                                                                                                                                                                                              Length 350;
                                                                                                                                 Indels
                                                                                                                                 0,
                                                                                                                                 Gaps
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292 ASFHSAVESLLKANNPWPAGSSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 350

61 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 119

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                                                                                                                                                                                                                                       PT New isolated nucleic acid encoding sub-units of liver activin -
proved nucleic acid encoding sub-units of liver activin -
proved nucleic acid encoding sub-units of liver activin -
proved nucleic acid encoding sub-units of cells, e.g. for
proved it reputating liver, bone and haematopoietic disorders

PS Claim 16; Fig 1; 141pp; English.

CC This represents a murine liver activin beta c polypeptide. Sequences
CC derived from beta c cDNA clone is used for screening and cloning a liver
CC activin beta e gene. Disorders of cell growth or differentiation (or
CC susceptibility to them) are diagnosed by measuring liver activin gene.
CC cartivity or by detecting a mutation in the liver activin gene. Disorders
CC of haematopoiesis, erythroid differentiation, ovarian follicular
CC differentiation, hormone secretion, neuronal survival, spermatogenesis, bone
CC differentiation, hormone secretion, neuronal survival, spermatogenesis, bone
CC differentiation can be stimulated by treatment with an liver activin
CC compound or agent that upregulates the compound's expression, antagonists
CC increase growth and regeneration of liver tissue. The liver activin
CC compound may also induce bone growth (e.g. for treating osteoporesis or
CC treating haemophilia, cystic fibrosis or menstrual disorders. Antibodies
CC are useful in immunoassays, to generate anti-idiotypic antibodies (which
CC transgenic animals containing liver activin gene can be used to produce
CC the liver activin receptors) and to inhibit liver activin. Also,
CC modulators
CC modulators
CC modulators
CC modulators
CC modulators
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Murine liver activin beta c polypeptide.

Liver activin; beta c; beta e; cell differentiation; haematopoiesis;

Liver activin; beta c; beta e; cell differentiation; heuronal survival;

erythroid; ovarian follicular maturation; hormone; neuronal survival;

spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis;

osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunoassay;

menstrual disorder; transgenic; modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-NOV-1997; U20882.
20-NOV-1996; US-752919.
(UNMI) UNIV MICHIGAN.
Bonadio J. Fang J;
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                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; V38237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W60617 standard; Protein; 352 AA.
W60617;
                                                              232 RVRRRGIDCQGASRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGIS 291
292 ASFHTAVLNLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGC 351
                                     1 RARRETTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 60
                                                                                                                                           Match 69.0%;
Local Similarity 63.6%;
                                                                                                                                                                                                            352 AA;
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
237. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-
161. .]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "mature growth factor domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Asn is putatively N-glycosylated'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'propeptide domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Asn is putatively N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Asn is putatively N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endoproteolytic cleavage site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Asn is putatively N-glycosylated'
                                                                                                                          Score 632; DB 1; Le pred. No. 3.36e-56; 26; Mismatches 16;
                                                                                                                                                                  Length 352;
                                                                                                                          Indels
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RESULTANT OF CASE AS A CORRESPONDED TO SERVICE O
RESULT
LD R.A.
AC I.I.
DT I.I.
DT X.
AC X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding transforming growth factor beta MP-121 - has mitogenic provided by transforming growth factor beta MP-121 - has mitogenic and differentiation-inducing activity, e.g. for use in wound healing PS Claim 7; Page 11; 15pp; German.

CR A cDNA library prepared using total RNA from human liver was subjected to PCR amplification using primers corresp. to conserved regions within the TGF-beta family. Amplification products were subcloned and sequenced; one clone (designated pSK-MP121) was found to contain a new sequence. Part of the insert from the clone was subcloned and sequence. Part of the insert from the clone was contain a new sequence. Part of the present sequence) was coding for a TGF-beta-like protein (i.e. the present sequence) was coding for a TGF-beta-like protein (i.e. the present action inducing properties making it (or fusion proteins comprising it or heterodimers of the protein with a cystine knot motif protein) useful for inducing tissue regeneration, e.g. for wound healing, inducing growth of the protein with a cystine knot motif protein, treating fertility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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04-JAN-1995; 011243.
27-MAR-1995; DE-423190.
01-JUL-1994; DE-423190.
(BIOP-) BIOPHARM GES BIOTEC!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-1996 (first entry)
09-AUG-1996 (first entry)
Transforming growth factor beta MP-121.
TGF-beta; MP-121; mitogen; differentiation; induction; promotion;
TGF-beta; MP-121; mitogen; recommendation; dental implantation;
                                       05-SEP-1990; 117079.

05-SEP-1989; JP-299250.

06-SEP-1989; JP-190774.

(TAKE ) TAKEDA CHEMICAL IND KK.
                                                                                                                                                                                                                                                                                                              Xenopus laevis
EP-416578-A.
                                                                                                                                                                                                                                                                                                                                                                                                   BMF; osteoporosis; fracture; cartilage
                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-MAY-1991 (first entry)
Xenopus Bone Morphogenetic Factor M3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R10991 standard; Protein; 127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      maintenance; morphogen; tissue regeneration; dental implantation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R89729 standard; Protein; 352 AA. R89729;
                                                                                                                                                                                                                                                                13-MAR-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 HRRGIDCOGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAAS 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294 FHTAVLNILKANTAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 S 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 63.9%; es 76; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ASEHSAVESLLKANNPW-PAS-TSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 FHSAVFSLLKANNPW-PAST-SCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 RRRTPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIAAS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96-050788/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIOTECHNOLOGISCHEN ENTWICKL. dt H, Pohl J, Hoetten G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 616; DB 1;
Pred. No. 1.93e-54,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
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(SCIT-) SCITECH RESEARCH CO

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RESULP PACES OF PACES
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                                                                                                                                                 SCCCCCCC PPT DRI
                               Matches
                                                                                     Query Match
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-APR-1986;
18-APR-1985;
06-SEP-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis bone morphogenetic protein and DNA encoding it used in therapy of fracture or osteoporosis
Claim 2; Fig 3; 28pp; English.

A Xenopus laevis liver-derived DNA library in Charon 28 vector, was screened with a rat activin beta-A cDNA probe. Five clones were isolated, including clone M3. They were subcloned in pUC19 and used to transform competent E.coli HB101 cells. Transformant E.coli HB101/pXar3 coding for the M3 BMP was sequenced and the amino acid sequence of M3 deduced from it.

See also Q10890 and Q10892-7.
                                                                                                                                                                                              Disclosure; Fig 8; 71pp; English.

DNA encoding inhibin and inhibin or part, analogues, homologues or precursors thereof when produced recombinant techniques are also precursors as well as pharmaceutical compositions thereof. These may be used as an inhibin agonist, antagonist or for eliciting an antigenic response to affect gonadal function or reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUN-1991 (first entry)
Sequence of human inhibin B subunit.
Hormone; inhibin agonist; antagonist;
                                                                                                                                           physiology.
Sequence 130 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SVIN-) ST VINCENTS'S INST MED Forage R, Stewart A, Robertson WPI: 86-291647/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HENRY'S HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MONU ) MONASH UNIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P60520 standard; Protein; 130 P60520;
                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide sequences and recombinant DNA - encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-APR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-MAY-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; Q10891.
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                                                                                                                                                                                                                                                                                                                                                                                                      inhibin and synthetic peptides useful for affecting gonadal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-OCT-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO8606076-A.
            54.48;
Local Similarity 45.58;
les 55; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RARRRIPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 HATKRSLNCDQNSNLCCRKDYYVDFKDIGWNDWIIKPEGYQINYCMGLCPMHIPGAPGTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86-291647/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSFHTTVLNLIKANNIQTAVNSCCVPTKRRPLSMLYFDRNNNVLKTDIADMIVEACGCS 127
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AU-003961.
AU-059039.
CN-103459.
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AU-002320.
AU-003157.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AU0097
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                               Score 498; DB 1;
Pred. No. 1.54e-41;
32; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 608; DB 1;
Pred. No. 1.46e-53;
27; Mismatches 21
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                                                                                     DB 1; Length 130;
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Best Local :
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(SVIN-) ST VINCENTS'S INST MED FOrage R, Stewart A, Robertson WPI; 86-291647/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure: Fig 6; 71pp; English.

DNA encoding inhibin and inhibin or part, analogues, homologues or precursors thereof when produced by recombinant techniques are also claimed, as well as pharmaceutical compositions thereof. These may be used as an inhibin agonist, antagonist or for eliciting an antigenic response to affect gonadal function or reproductive
   P70203 standard; protein; 426 AA
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Sequence of bovine inhibin B subunit.
Hormone; inhibin agonist; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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20-DEC-1985;
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                                                                                                                                                                                                                                                                                             228 LSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC 287
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                                                                                                                                                                                                                                                                                                                                                   1 RARRETPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polynucleotide sequences and recombinant DNA - encoding
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                                                                                                                                                                                                                                                                                                                                                                                                         RRRRGLECDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSS 227
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Similarity 45.5%;
55; Conservation
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AU-002320
AU-003157
AU-003960
AU-003961
AU-003961
AU-059039
CN-103459
AU-071015
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10-FEB-1986; US-827710.
12-SEP-1986; US-906729.
(GETH ) GENENTECH INC.
Mason AJ, Seeburg PH;
MPI, 87-137512/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 8A; 48pp; English.

A compsn. comprising human or porcine inhibin which is completely free of unidentified or porcine proteins is claimed. Also claimed are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta chain. Sequencing of inhibin-encoding cDNA has led to the identification of prodomain regions located N-terminal to the mature inhibin chains that represent coordinately expressed biologically active polypeptides. The prodomain regions or prodomain immunogens are useful in monitoring preproinhibin processing in transformant cell culture or in experiments directed
          8-JUL-1988; 170142.
9-MAR-1988; JP-055270.
(AJIN) Ajinomoto KK.
WPI; 90-055348/08.
                                                                                                                    27-JUL-1990 (first entry)
BUF-3 human differentiation inducing factor gene product.
BUF-3; dhfr; dihydrofolic acid reductase; differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant human or porcine inhibin or activin - used for modulating clinical condition or reproductive physiology of
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Sequence of human inhibin beta-chain precursor beta-A.
Fertility control; contraception; hormone; spermatogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 animals
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                                                                                             Homo sapiens.
J02009388-A.
                                                                                                                                                                        R05413;
                                                                                                                                                                                      R05413 standard; protein; 426 AA.
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                                                                         2-JAN-1990.
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311. .326
306. .310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 498; DB 1; Length 426; Pred. No. 1.54e-41; Indels 32; Indels
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Best Local Similarity
Matches 55; Conser
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Best Local :
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02-OCT-1986;
03-OCT-1985;
10-FEB-1986;
12-SEP-1986;
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Example 1; Fig 1; 12pp; Japanese.

Example 1; Fig 1; 12pp; Japanese.

Gene may be expressed by transforming a dhfr negative strain of CHO cells with an active BUF-3 gene and dhfr carrying vector. BUF-3 gene product is a cell differentiating factor.
                                                                                                                                                       Disclosure: Flg 2B: 48pp; English.

A compsn. comprising human or porcine inhibin which is completely free of unidentified or porcine proteins is claimed. Also claimed are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta chain. Sequencing of inhibin-encoding cDNA has led to the identification of prodomain regions located N-terminal to the mature inhibin chains that represent coordinately expressed biologically active polypeptides. The prodomain regions or prodomain immunogens are useful in monitoring preprinhibin processing in transformant cell culture or in experiments directed at modulating the climical condt. or reproductive physiology of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Physiologically active protein prepn. - physiologically by transforming plasmid having gene coding physiologically active protein and gene of di:hydrofolic acid reductase to hamster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-APR-1991 (first entry)
Sequence of porcine inhibin beta-chain precursor beta-A.
Fertility control; contraception; hormone; spermatogenesis.
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                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; N70317
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307 RRRRRGLECDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSS 366
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                                                                                                                             427 AA;
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US-783910.
US-827710.
US-906729.
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                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="proteolytic processing site
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45.5%;
                                                    Score 498; DB 1; Length 427
Pred. No. 1.54e-41;
32; Mismatches 32; Indels
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Pred. No. 1.54e-41;
32; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32;
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RESULT
AC R
AC R
DT 1:
DE X
KW BB
OS X
PN E
PD 1:
PD 1:

BMF;

xenopus

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427

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Query Match
Best Local Similarity
14-MAY-1991.
24-JUN-1988; US-878063.
23-JUN-1988; US-878063.
23-JUN-1988; US-210683.
23-JUN-1988; US-710683.
SPIESS J. RIVIET FOR BIOL STUD.
SPIESS J. RIVIET JEF, Bardin CW, Vale WW;
WPI: 91-163615/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; Q10890.

N-PSDB; Q10890.

Xenopus laevis bone morphogenetic protein and DNA encoding it weed in therapy of fracture or osteoporosis

Claim 2; Fig 3; 28pp; English.

A Xenopus laevis liver-derived DNA library in Charon 28 vector, was screened with a rat activin beta-A cDNA probe. Five clones were isolated, including clone 89. They were subcloned in pUC19 and used to transform competent E.coli HB101 cells. Transformant E.coli HB101/pXar9 coding for the 89 BMP was sequenced and the amino acid sequence of 89 deduced from it.

See also Q10891-7.
                                                                                                                                                                                                                                                                                                                                                        Follicle stimulating hormone; FSH; fertility; gonadotropin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R12088 standard; Protein; 116 AA.
R12088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TAKE ) TAKEDA CHEMICAL IND KK. (SCIT ) SCITECH RESEARCH CO. MURAKAMI K, UGNO N, KATO Y; WPI; 91-075112/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-MAR-1991.
05-SEP-1990; 117079.
06-SEP-1989; JP-229250.
20-JUL-1990; JP-190774.
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1991 (first entry)
                                                                                                                                                                                                                                                                                                                          Crambe abyssinica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-MAY-1991 (first entry)
Xenopus Bone Morphogenetic Factor B9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R10990 standard; Protein; 130 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ASFHSAVFSL--LKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGC 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 LSFHSTVINOYRLRGOSPFTSIKSCCVPSKLRAMSMLYYDDGQNIIKKDIQNMIVEECGC 129
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Pred. No. 3.09e-40;
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PS Claim 1; Page 11; 11pp; English.

CC The sequence is the N-terminal of the 16.5 kD subunit of the ovine control of the secretion of the control o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Determination of activin using anti-activin antibody - for the diagnosis of megakaryocyte thrombocytopaenia Disclosure; Page 16: 18pg, Japanese.

The peptide shown is an activin-like peptide which was used to demonstrate a method of detecting activin and/or an activin-like substance using an antibody recognising all or part of activin. The method comprises an enzyme immunoassay, RIA, chemilumino-assay, fluoro-immunoassay or time resolved fluorescence immunoassay, fluoro-immunoassay or time resolved fluorescence immunoassay the index of coagulation of latex grain to erythrocyte. The measurement of activin and/or activin-like substance is useful for the diagram of activin and/or activin-like substance is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-DEC-1990; 409591.
28-DEC-1990; JF-409591.
(MOCH ) MOCHIDA PHARM CO LTD.
WPI; 92-327039/40.
        P80019 standard; Protein; 116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the diagnosis of megakaryocyte thrombocytopaenia. See also R26480-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Activin-like peptide.
Anti-activin antibody; diagnosis; megakaryocyte thrombocytopaenia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pure ovine inhibin protein - which inhibits secretion of follicle stimulating hormone while not inhibiting secretion of luteinising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.1%;
Local Similarity 46.0%;
nes 52; Conservation
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                                                                                                                                                                                                                                     64 NHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGENIIKKDIENMIVEECGCS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 45.1%; les 51; Conservative
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                                                                                                                                                             S-L-LKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.0%;
45.1%;
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Pred. No. 3.76e-39;
32; Mismatches 28;
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Pred. No. 2.93e-39;
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Matches

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                                                                                                                                                                                                                             Query Match 51.5%;
Best Local Similarity 45.1%;
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                      Rivier JEF, Valew;

WPI: 88-119128/17.

New proteins with inhibin activity - esp. useful for controlling fertility in males
Claim 1; Column 7-8; 6pp; English.

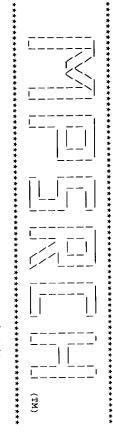
Claim 1; Column 7-8; 6pp; English.

The inventors claim 2 proteins - A and B - each of which has a molecular weight of about 32K and is comprised of an alpha (18K) and a beta (14K) chain of human inhibin. The alpha chain is p80018.

The beta chain is either P80019 or P80020. Proteins A and B are useful for regulating fertility of mammals. Each 32K protein exhibits inhibin activity in basal secretion of FHS but not inhibiting basal secretion of luteinizing hormone (LH).

Sequence 116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
US4737578-A.
12 APR-1988.
12 APR-1986; US-8284.
10 FEB-1986; US-828435.
07-APR-1986; US-828435.
07-APR-1986; US-828924.
(SALK ) SALK INST FOR BIOL STUD.
EVANS RM, Rosenfeld MG, Cerelli G, Mayo KE, Spiess J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P80019;
28-JAN-1993 (first entry)
Sequence of the 14K beta-chain of a protein exhibiting
inhibin activity.
Fertility control; inhibin; follicle stimulating hormone; inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gonadotropin.
                                                                              69 S-L-LKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 119
                                                                                                  4 CDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVI 63
                                                                                                                                                       9
                                                                                                                                                       CEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIAASFHSAVF 68
                                                                                                                                                                                                                               Score 472; DB 1; Length 116; Pred. No. 1.02e-38; 32; Mismatches 28; Indels
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srch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Aug 17 10:16:03 2000; MasPar time 8.90 Seconds 630.799 Million cell updates/sec

Tabular output not generated.

Title:

Description:
Perfect Score:
Sequence: >US-08-765-662-12 (1-119) from 5929213.pep 916 1 RARRRIPTCEPATPLCCRRD......NGNVVKTDVPDMVVEACGCS 119

Scoring table: PAM 150 Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir64 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 39.770; Variance 63.509; scale 0.626

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query	Length	BB	ID	Description	Pred. No.
٠	906		350	2	JC5241	activin beta E chain	.86e-20
2	632	69.0	352	N	S70580	activin beta C precur	e-1
ω	629		352	N	JC5366	activin beta C - mous	.16e-12
4	619		367	N	JC4151	activin beta D chain	.13e-12
u	616		352	N	JC2466	inhibin beta-C chain	.59e-12
თ	503		425	N	147072	inhibin beta-A chain	
7	498		424	Н	WFPGBA	inhibin beta-A chain	.11e-
œ	498		424	Ļ	S31440	inhibin beta-A chain	.11e-9
9	498	54.4	425	۳	S50898	beta-A	÷
10	498		426	\vdash	B24248	beta-A	.11e-9
11	487		424	<u>بــ</u>	B40905	beta-A	.95e-9
12	474	:	370	ν	I51199	beta B sub	0e-8
13	472	51.5	413	N	JC4862	beta-A cha	1.68e-88
14	471	:	255	N	I48235	beta-B	8e-8
15	471	51.4	411	N	B41398	in beta-B cha	8-98
16	468	-	349	-ب	WFPGBB	in beta-B	8-9B
17	468	51.1	407	_	A40150	beta-B	1.686-8
18	468	:	408	N	S50899	nhibin pre	1.68e-8
19	464	۲.	393	N	I50103	beta B - zeb	1.6/e-8
20	442	۳.	115	N	PN0506	activin beta B-2 chai	5.06e-8
21	. 441	48.1	115	N	PN0505	beta B-	8.97e-8
22	436		115	N	PN0504	beta A	O,
23	402		102	2	A36192	inhibin beta-A chain	4.00e-/1

45	44	43	42	41	40	39	38 8	37	36 6	ω Çī	34	ယ	32	31	30	29	28	27	26	25	24
327	327	331	331	333	339	341	346	350	350	350	351	352	352	352	352	352	352	3 5 5	355 5	386	388
35.7	35.7	36.1	36.1	36.4	37.0	37.2	37.8	38.2	38.2	38.2	38.3	38.4	38.4	38.4	38.4	38.4	38.4	38.8	38.8	42.1	42.4
510	207	513	360	373	408	372	35 35	396	394	393	405	420	408	408	408	401	400	398	398	101	101
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Vg-1-related protein	- rac (bone morphogenetic pr	Vgl embryonic growth	activin - fruit fly (bone morphogenetic pr	GDF-1 embryonic growt	bone morphogenetic pr					bone morphogenetic pr	inhibin beta-Bl chain	beta-B2							
7.34e-53		. ove	. oue	. 64e-5	9.426-56	. Lue-5	. 91e-5	່, ບໍ່	.056-5	.05e-	.1/e-5	ιĠ	ינו טינו	- 92	2e-5	2e-5	ιċ	່ເປ	່ເປ	ιď	.10e-

ALIGNMENTS

Db 292 ASFHS!	Db 232 RARRRI Qy 1 RARRRI	Query Match Best Local Sim Matches 116;	#introns CLASSIFICATION SUMMARY	Ac	##resiques COMMENT This Sup	#cross-references MUID #accession JC5367 #molecule_type DNA	#journal #title	REFERENCE #authors	##residues	#accession JC5241 ##molecule_type mRNA	#CFOSS-refere	#authors #journal #title	ACCESSIONS REFERENCE	ENTRY TITLE ORGANISM DATE	RESULT 1
ASFHSAVFSLLKANNPWPAGSSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 350	RARRRTPTCEPETPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 291 	Query Match 98.9%; Score 906; DB 2; Length 350; Best Local Similarity 97.5%; Pred. No. 8.86e-200; Matches 116; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	99/3 #superfamily inhibin #length 350 #molecular-weight 39057 #checksum 2625	different combination of beta subunits. Activin beta C and beta E form a distinct subset of related activins.	##rcstautes 1.300 ##.dbeir FA.4 ##cross-references GB:U96386; NID:92072521; PID:92072522 This protein is a member of the transforming growth factor-beta superfamily. There are three activins, A, B, and AB consisting of	nces JC53	Biochem. Biophys. Res. Commun. (1997) 231:000-001 Genes coding for mouse activin beta C and beta E are closely linked and exhibit a liver-specific expression pattern in adult tissues	Fang, J.; Wang, S.; Smiley, E.; Bonadio, J.	##residues 1-350 ##label FAN ##cross-references GB:U96386; NID:g2072521; PID:g2072522	JC5241 Ltype mRNA		Fang, J.; Yin, W.; Smiley, E.; Wang, S.Q.; Sounding, G. Biochem. Biophys. Res. Commun. (1996) 228:669-674 Molecular cloning of the mouse activin beta E subunit gene.		<pre>JC5241 #type complete activin beta E chain precursor - mouse #formal_name Mus musculus #common_name house mouse 25-Apr-1997 #sequence_revision 09-May-1997 #text_change 26-Auq-1999</pre>	

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232 RVRRRGIDCQGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGIS 291
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##residues 1-352 ##label FAN
##cross-references GB:U95962
WT Activin beta C and beta E fo
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Similarity 63.6%;
77; Conservation
                                        Similarity 76; Conser
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                                                                                                      #superfamily #length 352
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Biophys. Res. Commun. (1997) 231:655-661
Genes coding for mouse activin beta C and beta E are closely
linked and exhibit a liver-specific expression pattern in
adult tissues.
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#formal_name Mus musculus #common_name house mouse

28-May-1997 #sequence_revision 18-Jul-1997 #text_change
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activin beta C precursor - mouse
#formal_name Mus muscullus #common_name house mouse
14-Feb-1997  #sequence_revision 13-Mar-1997  #text_change
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                                    Score 629; DB 2;
Pred. No. 3.16e-1
27; Mismatches
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     ##cross-references GB:X82540;
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Similarity 62.2%;
74; Conservation
                                                                                                                                                                                                          inhibin beta-C chain precursor - human activin beta C chain precursor - human #formal_name Homo sapiens #common_name man 29-Mar-1995 #sequence_revision 26-May-1995 #text_change
                                                                                       Hoetten, G.; Neidhardt, H.; Schneider, C.; Pohl, J. Biochem. Biophys. Res. Commun. (1995) 206:608-613 Cloning of a new member of the TGF-beta family: A putative new activin betaC chain.
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JC2466
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predicted
#length 367 #molecular-weight 41729 #checksum 2774
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activin beta D chain precursor - African clawed frog
#formal_name Xenopus laevis #common_name African clawed
27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change
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#product activin beta D chain #status predicted #label
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PIDN:CAA57890.1; PID:g669155
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110,143,161
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#journal Mol. Reprod. Dev. (1995) 40:1-8

#title Tissue-specific variation in the length of the
untranslated region of the beta A-inhibin mRN
#cross-references_MUID:95217464
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##molecule_type protein
##residues
310-312,'x',314-319,'XX',322 ##label LEV
##residues
Inhibin suppresses follicle-stimulating hormone secretion.
IFICATION
#superfamily inhibin
#superfamily inhibin
disulfide bond; glycoprotein; gonad; heterodimer; hor
RRDS
#length 425 #molecular-weight 47565 #checksum 2083
                                                                                                                                                                                                                                                                                                                                                                                                        ##cross-references GB:L19218; NID:g310379; PIDN:AAC41621.1; PID:g310380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##experimental_source liver
This protein is a member of the TGF-beta superfamily, activins
compose of homo or heterodimers of the beta A and beta B chain.
                       305 RRRRRGLECDGKVNICCKKQFTVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSS 364
                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 HRRGIDCQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAAS 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##cross-references GDB:632884
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                                                                                            Local
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   RARRRTPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 60
                                                                      54.9%;
Similarity 46.3%;
56; Conservation
                                                                                                                                                                                                                                                                B60856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147072 #type complete
1147072 #type complete
#formal_name Ovis orientalis aries, Ovis ammon aries
#common_name domestic sheep
15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change
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#length 352 #molecular-weight 38238 #checksum 8314
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#domain propeptide #status predicted #label PRO\
#product activin beta C #status predicted #label MAT\
#binding_site carbohydrate (Asn) (covalent) #status
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                                                                      Score 503; DB 2; Lend
Pred. No. 2.83e-96;
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Pred. No. 6.59e~125;
26; Mismatches 15;
                                                                                                            Length 425;
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ACCESSIONS REFERENCE

A60087; A60087

I48265; S31440

10-Sep-

ALTERNATE_NAMES
ORGANISM

\$31440 #type complete
inhibin beta-A chain - mouse
activin A; mesoderm-inducing factor WEHI-MIF
#formal_name Mus musculus #common_name house mouse
10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change

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RESULT
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21-308
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#journal Nature (1985) 318:659-663

*title Complementary DNA sequences of ovarian follicular fluinhibin show precursor structure and homology with transforming growth factor-beta.

#cross-references MUID:86092207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165
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NT The source of this protein is ovarian follicular fluid.
NT The mature protein is the carboxyl-terminal segment of a precursor polypeptide; the active molecule is a dimer of one beta and one alpha chain, linked by one or more disulfide bonds. Two different forms of inhibin have been isolated (A and B) that differ in the amino-terminal sequence of their beta chains.

TI Inhibin is secreted by ovaries or testes and inhibits the secretion of follitropin by the pituitary gland.

FICATION #superfamily inhibin DS
                                                                                       119
                                                                                                                               424 S 424
                                                                                                                                                                                                                    364 LSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC 423
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Local Similarity 45.5%;
hes 55; Conservative
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13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change
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Pred. No. 5.11e-95;
32; Mismatches 32
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                                       #authors Forage, R.G.; Ring, J.M.; Brown, R.W.; McInerney, B.V.;
Cobon, G.S.; Gregson, R.P.; Robertson, D.M.; Morgan, F.J.;
Hearn, M.T.W.; Findlay, J.K.; Wettenhall, R.E.H.; Burger,
H.G.; De Kretser, D.M.

#journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:3091-3095
#title Cloning and sequence analysis of cDNA species coding for the
#title two subunits of inhibin from bovine follicular fluid.
#cross-references MID:86205842
                                                                                                                                                                                                                                                                                                                                                                                                                    #title beta(A)- and beta(B)-inhibin/activin genes. Identification function factor AP-2-binding sites in the scross-references MUID:95112839
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##residues 309-311,'X',313-318,'XX',321-325 ##label
##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                           ##molecule_type DNA
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Local Similarity 45.5%;
pes 55; Conservative
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Development (1990) 110:435-443
A mesoderm inducing factor produced by WEHI-3 murine myelomonocytic leukemia cells is activin A.
nces MIID:92155098
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Activins are expressed in preimplantation mouse embryos and in ES and EC cells and are regulated on their
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Best Local :
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310-425
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#title
                                            subunit gene. #cross-references MUID:92135888
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#journal Mol. Cell. Endocrinol. (1986) 44:55-60
#title Isolation of bovine follicular fluid inhibin of about 32 kDa
#cross-references MUID:86136989
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#accession A60960
##molecule_type protein
##residues 310-312,'X',314-319,'XX',322-328,'P' ##label CHE
                        #accession
                                                                                                                    #journal
                                                                                                                                                                 #authors
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  ##status
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##residues 310-313 ##label FUK
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Local Similarity 45.5%;
Local Similarity 45.5%;
hes 55; Conservative
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Inhibin beta-A chain precursor - human
activin A; activin AB chain A; erythroid differentiation
factor; megakaryocyte differentiation active protein
#formal_name Homo sapiens #common_name man
10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
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Mesoderm-inducing factor from bovine amniotic fluid:
purification and N-terminal amino acid sequence
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disulfide bond; glycoprotein; gonad; heterodimer; homodimer;
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                                                                                         Structure and sequence analysis of the human activin beta(A)
                                                                                                                                                                 Tanimoto, K.; Handa, S.I.; Ueno, N.; Murakami, K.; Fukamizu,
                                                                                                                                                                                                           S30488; B23556; B24248; A30884; S33351; PN0010
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#domain propeptide #status predicted #label PRO\
#product beta-A inhibin/activin #status experimental
preliminary
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Pred. No. 5.11e-95;
32; Mismatches 32
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                                                                                                     FEATURE
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#title Biochem. Biophys. Res. Commun. (1991) 174:1163-1168

#title purification of megakaryocyte differentiation activity from a human fibrous histiocytoma cell line: N-terminal sequence homology with activin A.

#cross-references MUID:91144591
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#title Erythroid differentiation factor is encoded by the same mRNA
as that of the inhibin beta-A chain.

#cross-references_MUID:88190086
                                                                                                                                                                                                        #map_position 7p15-7p13
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#journal FEBS Lett. (1986) 206:329-334
#title Human inhibin genes. Genomic characterisation and sequencing.
#cross-references MUID:87005283
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                                                                                                                                                                                                                                                                                                  ##molecule_type protein

311-313,'X',315-320,'XX',323-328,'X',330-334 ##label FUJ

##residues

311-313,'X',315-320,'XX',323-328,'X',330-334 ##label FUJ

NT Activins A and B are homodimers of inhibin beta-A or inhibin

beta-B, respectively, while activin AB is a heterodimer. Inhibins

A and B are heterodimers of the inhibin alpha chain with inhibin

beta-A and beta-B, respectively.
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##cross-references EMBL:X87578; NID:g28351; PIDN:CAA40805.1; PID:g825621
##note the authors translated the codon GAG for residue 53 as
Gly and GAG for residue 56 as Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues 311-375,'AC', 380-426 ##label BER ##cross-references EMBL:X72498; NID:g297786; PIDN:CAA51163.1; PID:g755740
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NCE A30884
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Biochem. Biophys. Res. Commun. (1986) 135:957-964
Structure of two human ovarian inhibins.
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*product inhibin beta A chain *status experimental *label MAT\
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Best Local Similarity 45.5%;
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#title
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#title Complementary deoxyribonucleic acid (cDNA) cloning and DNA #cross references MUD:90331931
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##status
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##cross references GB:M37482; NID:g204936; PIDN:AAA41436.1; PID:g204937
FICATION #superfamily inhibin
YY #length 424 #molecular-weight 47356 #checksum 1734
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119 S 119
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                                                                                                                                                                                                                                                                              y Match 53.2%;
Local Similarity 44.6%;
hes 54; Conservative
                                                                                          61 ASFHSAVFS-L-LKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGC 118
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A40056
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#length 426 #molecular-weight 47442 #checksum 3853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Woodruff, T.K.; Meunier, H.; Jones, Mayo, K.E.
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#formal_name Rattus norvegicus #common_name Norway rat
10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
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0905; B40056
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Pred. No. 5.11e-95;
32; Mismatches 32;
                                                                                                                                                                                                                                                                           Score 487; DB 1;
Pred. No. 2.95e-92;
32; Mismatches 33
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st Local Similarity 48.3%;
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This protein is secreted from Sertoli cells and plays a role in the
regulation of newt spermatogenesis.

(FICATION #superfamily inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##residues 1-413 ##label YAM
##cross-references GB:D84516; NID:g1502288; PIDN:BAA12693.1;
PID:d1013374; PID:g1502289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 RIRKRGLECDGHTNLCCRQQFYIDFRLIGWNDWIIAPAGYYGNYCEGSCPAYLAGVPGSA 310
                                             353 PSFHAAVINQYRMRGYSPFTSVKSCCVPTKLRAMSMLYYDDGQNIIKKDIQNMVVEECGC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 SSFHTAVVNQYRMRGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVDECGCA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues 1-370 ##label DOH
##cross references GB:561773; NID:g386027; PIDN:AAB26863.1; PID:g386028
FICATION #superfamily inhibin
# #length 370 #molecular-weight 41678 #checksum 6606
                                                                                                                                               293 RRRKRGLECDGKVSICCKKQFYVSFKDIGWSDWVIAPPGYTANYCEGDCPMYITGTSGSG 352
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61' ASFHSAVFSL--LKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGC 118
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Local Similarity 43.0%;
                                                                                                 1 RARRRIPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 60
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Biochem. Biophys. Res. Commun. (1996) 224:451-456
Expression of activin beta subunit genes in sertoli cells of
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Dev. Biol. (1993) 157:474-483
Expression of activin mRNA during early development in Xenopus laevis.
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activin bene-Kohain precursor - newt
#formal_name Cynops pyrrhogaster #common_name newt
15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change
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#product activin beta-A chain #status predicted #label
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                                                                                                                                                                                          Score 472; DB 2;
Pred. No. 1.68e-88;
33; Mismatches 34
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#title Activins are expressed in preimplantation mouse embryos and in ES and EC cells and are regulated on their differentiation.
#cross-references MUID:93321614
#accession 148266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 51.4%;
Best Local Similarity 48.3%;
Matches 58; Conservative
                                                                                                              #authors
#journal
#title
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#journal Mech. Dev. (1995) 50:229-245

#title Activin disrupts epithelial branching morphogenesis

#cross-references MUID:95344997
                                   #cross-references MUID:90190649
#accession B41398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 RIRKRGLECDGRTSLCCRQQFFIDFRLIGWNDWIIAPTGYYGNYCEGSCPAYLAGVPGSA 195
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##molecule_type DNA
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inhibin beta-B chain precursor - rat
inhibin/activin beta B-chain
#formal_name Rattus norvegicus #common_name Norway rat
97-py-1992 #sequence_revision 01-Aug-1997 #text_change
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                                                                              A41398
Feng, Z.M.; Li, Y.P.; Chen, C.L.C.
Feng, Z.M.; Li, Y.P.; Chen, C.L.C.
MO1. Endocrinol. (1989) 3:1914-1925
Analysis of the 5'.flanking regions of rat inhibin alpha-
Analysis of the 5'.flanking regions of different regulatory
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02-Jul-1996 #sequence_revision 01-Aug-1997 #text_change
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Pred. No. 2.98e-88;
27; Mismatches 3;
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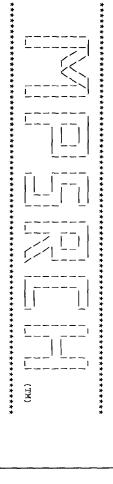
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##status preliminary; not compared with conceptual translation
##molecule_type mRNA
##residues 133-411 ##label ESC
CLASSIFICATION #superfamily inhibin
SUMMARY #length 411 #molecular-weight 45182 #checksum 2167
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Search completed: Thu Aug 17 10:16:42 2000 Job time: 39 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##molecule_type DNA ##label RES 1-7 ##label RES ##cross-references GB:572477; NID:g619268

##across-references GB:572477; NID:g619268

##across-references GB:572477; NID:g619268
                                                                                                                                                                                                                                                                                                                                                    Query Match 51.4%;
Best Local Similarity 48.3%;
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors Esch, F.S.; Shimasaki, S.; Cooksey, K.; Mercado, M.; Mason, A.J.; Ying, S.Y.; Ueno, N.; Ling, N.
#journal Mol. Endocrinol. (1987) 1:388-396
#title Sequence analysis of rat ovarian inhibins.
#cross-references MUID:90331931
#accession C40905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors
#journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cells.
#cross-references MUID:94307180
#accession 153288
                                                                                                                                                                                                                                                                   292 RIRKRGLECDGRTSLCCRQQFFIDFRLIGWNDWIIAPTGYYGNYCEGSCPAYLAGVPGSA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##residues 1-174 ##label FEN 1-176 ##cross-references GB:M32756; GB:M32757; NID:g204943; PIDN:AAA41438.1; PID:g554460
                                                                                                                                                                        352 SSFHTAVVNQYRMRGLNPGPVNSCCIPTKLSSMSMLYFDDEYNIVKRDVPNMIVEECGCA 411
                                                                                                             61 ASEHSAVESLIKANNPWPAST-SCCVPTARRPLSLLYLDHNGNVVKIDVPDMVVEACGCS 119
                                                                                                                                                                                                                                    1 RARRRIPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dykema, J.C.; Mayo, K.E.
Endocrinology (1994) 135:702-711
Two messenger ribonucleic acids encoding the common beta
B-chain of inhibin and activin have distinct 5'-initiation
sites and are differentially regulated in rat granulosa
                                                                                                                                                                                                                                                                                                                                                    Score 471; DB 2; Length 411; Pred. No. 2.98e-88; 27; Mismatches 34; Indels
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srch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Thu Aug 17 10:20:47 2000; MasPar time 22.82 Seconds 531.656 Million cell updates/sec

Description: Perfect Score: >US-08-765-662-12 (1-119) from 5929213.pep

Sequence: 916
1 RARRETPTCEPATPLCCRRD.....NGNVVKTDVPDMVVEACGCS 119

Scoring table: Gap 11 PAM 150

714576 seqs, 101934467 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-pending 1:PCT 2:U6 3:U60 4:U7 5:U80 6:U81 7:U82 8:U83 9:U84A 10:U848 11:U85 12:U86 13:U87 14:U88 15:U89 16:U90 17:U91 18:U92 19:U93 20:U94 21:U95 22:NEWP 23:NEWU60 24:NEWU7 25:NEWU8 26:NEWU9

Statistics: Mean 32.690; Variance 102.861; scale 0.318

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	Score	% Query Match I	Length DB	ID	Description	On	Pred. No.
1	916	100.0	119 8	US-08-311-	Sequence	12, Applicati	4.26e-104
N	916	00.	119 17	US-09-184-	Sequence	•	4.26e-104
w	916	00.		US-08-274-	Sequence	-	4.26e-104
4	916	•		US-60-186-	Sequence	2	4.26e-104
υı	916	100.0		US-60-185-	Sequence	`	4.26e-104
o,	916	•		US-60-212-	Sequence	-	4.26e-104
7	916	100.0		us-09-521-	Sequence	4, Applicatio	4.26e-104
8	916	100.0		US-08-311-	Sequence	14, Applicati	4.26e-104
9	913	99.7	350 13	US-08-752-	Sequence	Applicatio	1.07e-103
10	906	98.9		US-08-752-	Sequence	13, Applicati	.23e-
11	906	98.9		us-08-752-	Sequence	 Applicatio 	9.23e-103
12	818	89.3		us-60-162-	Sequence	4023, Applica	4.97e-91
13	818	89.3		us-60-169-	Sequence	-	4.97e-91
14	806	88.0		US-60-163-	Sequence	1750, Applica	.96e-8
15	632	69.0		us-08-752-	Seguence	Applicatio	.10e-6
16	629	68.7	247 13	US-08-752-	Sequence	11, Applicati	5.20e-66
17	629	68.7		US-09-218-	Sequence	 Applicatio 	5.20e-66
18	629	68.7		US-08-981-	Sequence	4, Applicatio	5.20e-66
19	629	68.7		US-08-482-	Sequence	 Applicatio 	.20e-
20	629	68.7	352 12	US-08-679-	Sequence	4, Applicatio	.20e-

45	44	43	42	41	40	39	38	37	ω 6	<u>ω</u> 5	34	ω G	32	<u>ω</u>	30	29	28	27	26	25	24	23	22	21
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122	122	122	122	122	122	122	121	121	121	121	106	106	106	106	352	352	352	352	352	352	352	352	352	352
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence										
17,	27,	27,	23,	17,	45,	17,	19,	19,	19,	21,	7,	28,	28,	28,	2	2,		Ψ	4,	4,	4	4	-	ž
Applicati	Applicatio	Applicati	Applicati	Applicati	Applicatio	, Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	licat	Applicatio	\vdash										
.09e-4	7.09e-49	.09e-4	.09e-4	.09e-4	.09e-4	4	.09e-4	.09e-4	.09e-4	.09e-4	.74e-6	.74e-6	.74e-6	.74e-6	.49e-6	6	.67e-	.67e-6	.67e-	.67e-	.67e-6	.67e-	o	.67e-

ALIGNMENTS

RESULT US-08-311-370A-12 STANDARD; PRT; 119 AA.

Sequence 12, Application US/08311370A

Sequence 12, Application US/08311370A
GENERAL INFORMATION:
APPLICANT: LEE, SE-JIN
APPLICANT: LSQUELA, AUBORA F.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS:

ADDRESSEE: Los Angeles E: Spensley Horn Jubas & Lubitz 1880 Century Park East, Suite 500

COUNTRY: 90067 9 RF-CA

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSED VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,
FILING DATE: 26-SEP-1994 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette US/08/311,370A

APPLICATION NUMBER: 08/274,215
FILING DATE: 13-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A CLASSIFICATION: 435 PRIOR APPLICATION DATA:

NAME: Haile, Ph.D., Lisa A REGISTATION NUMBER: 38,347 REFERENCE/DOCKET NUMBER: PD-3830 TELECOMMUNICATION INFORMATION: TELEPHONE: 619-455-5100 619~455-5110

INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

12:

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Best Local :
 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/09184933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/09184933
                                         TELEFAX: 619-68-5099
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 119
                                                                                                               APPLICATION NUMBER: 08/274.21
FILING DATE: 13-ULI-1994
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D., Lisa A.
REGISTRATION NUMBER: 38.347
REFERENCE/DOCKET NUMBER: 0726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 119
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Local Similarity 100.0%;
es 119; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lee, Se-Jin
APPLICANT: Esquela, AUTOTA F.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 12
      MOLECULE TYPE: protein FRAGMENT TYPE: internal JENCE 119 AA; 13161 MW; 75307 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE: internal ORIGINAL SOURCE: JENCE 119 AA; 13161 MW; 75307 CN;
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
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STRANDEDNESS: single
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SYSTEM: Windows95
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                                                                                                                                                                                                                                                                                                             Diskette
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Pred. No. 4.26e-104;
0; Mismatches 0;
                                                                                                                                         07265/040001
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Best Local S
Matches 11
                                                                                                         Matches
                                                                                                                                  Query Match
                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/08274215
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Esquela, Aurora F.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ASFHSAVESLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 100.0%;
Local Similarity 100.0%;
les 119; Conservative
 61 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 119
               61 ASF3SAVFSLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 119
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                                                                                                                    Match 100.0%;
Local Similarity 100.0%;
                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: not relevan
TOPOLOGY: both
MOLECULE TYPE: protein
OUDNCE 119 AA; 13161 MW; 753
                                                                                                                                                                                                                                                         TELEFAX: 212/258-2291
INFORMATION FOR SEQ ID NO: 12:
                                                                    1 RARRRIPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RARRETPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RARRRTPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 60
                                                     1 RARRETPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA
                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212/765-5070
                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400
                                                                                                         119;
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CA
                                                                                                         Conservative
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                                                                                                                                                                                                     not relevant
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                                                                                                       Score 916; DB 7; L
Pred. No. 4.26e-104;
0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                         38,347
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Pred. No. 4.26e-104;
0; Mismatches 0;
                                                                                                                                                               75307 CN;
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Best Local Similarity 100.0%;
                                                                 Query Match
Best Local (
                                                     Matches
                                                                                                  FILE REFERENCE: CL000291
CURRENT APPLICATION NUMBER: US/50/185,361
CURRENT FILING DATE: 2000-02-28
NUMBER OF SEO ID NOS: 968
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 608
LENGTH: 153
TYPE: PRT
ORGANISM: HUMAN
SEQUENCE 153 AA; 16813 MW; 120970 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-60-186-656-992
                                                                                                                                                                                                                                                                                                                                                                                             XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: HUMAN
SEQUENCE 131 AA; 14330 MW; 90159
                                                                                                                                                                                                                                                                                                                                      Sequence 608, Application US/60185361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/60/186,656
CURRENT FILING DATE: 2000-03-03
NUMBER OF SEO ID NOS: 1518
SOFTWARE: FastSEQ for Windows Version 4.0
SEO ID NO 992
LENGTH: 131
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 992, Application US/60186656
                                                                                                                                                                                                                                                                                               Sequence 608, Application US/60185361 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 RARRRTPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000320
                                                                                                                                                                                                                                        APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING F
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               RARRRTPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RARRRIPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 60
  RARRETPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119;
                                                    h 100.0%;
Similarity 100.0%;
119; Conservative
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                                                    Score 916; DB 3; I
Pred. No. 4.26e-104;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 916; DB 3; L
Pred. No. 4.26e-104;
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                                                                               Length 153
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                                                                                                                                                                                                                                                          HUMAN SECRETED PROTEINS,
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Best Local S
Matches 11
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US-60-212-356-257
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                 SEQUENCE
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                                                                                                                                                                                                                                                                       Sequence 4, Application US/09521978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 RARRRIPICEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Beasley,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                 APPLICANT: Arterburn, Matthew C.
TITLE OF INVENTION: Methods And Materials Relating To
TITLE OF INVENTION: Activin/Inhibin-Like Polypeptides
FILE REFERENCE: HYS-2
CURRENT APPLICATION NUMBER: US/09/521,978
CURRENT FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 257
LENGTH: 274
                                                                                                                                                                                                                                                                                                                                                                                                                         216 ASFHSAVESLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 257, Application US/60212356 GENERAL INFORMATION:
                                                                                                                                                                                                                              Sequence 4, Application US/09521978 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 274
TYPE: PRT
ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: CL000677
CURRENT APPLICATION NUMBER: US/60/212,356
CURRENT FILING DATE: 2000-06-19
                                                                                                                                                                                      APPLICANT: Ford, John E.
APPLICANT: Mize, Nancy K.
APPLICANT: Dickson, Mark C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                                                                                                                                          61 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS
              LENGTH: 350
TYPE: PRT
ORGANISM: Homo sapiens
QUENCE 350 AA; 38561 MW; 616706 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RARRRIPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS
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1 Similarity 100.0%;
119; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
PROTEINS, AND USES THEREOF
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Pred. No. 4.26e-104;
0; Mismatches 0;
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Length 274; Indels

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                        Matches
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Best Local :
                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/08311370A
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23, RARRRTPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/08311370A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 RARRRTPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 350
                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 350 amino acids
                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/274,215
FILING DATE: 13-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D., Lisa A
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 9D-3830
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                 Local
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                                                                   FRAGMENT TYPE: internal ORIGINAL SOURCE: JENCE 350 AA; 38561 MW; 616706 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LEE, SE-JIN
APPLICANT: ESQUELA, AURORA F.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 14
                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                       ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                         STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 26-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                     h 100.0%;
Similarity 100.0%;
119; Conservative
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Similarity 100.0%;
119; Conservative
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1880 Century Park East, Suite 500
                                                                                                                                     linear
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                    Score 916; DB 8; L
Pred. No. 4.26e-104;
0; Mismatches 0;
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                     0;
                                           Length 350;
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         RESULT
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Best Local Similarity 99.2%;
Matches 118; Conservative
US-08-752-919-13
                                                                                                                                                                                                       SEQUENCE
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                                                                                                                  232 RARRRTPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGGPGIA 291
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GENERAL INFORMATION:
                                                                          292 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           292 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGGS 350
                                                 61
                                                                                                                                                                                                                                                                                  TELEPHONE: 212-790-909
TELEFAX: 212-869=8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                    1 RARRRIPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 60
                                                                                                                                                                                                                    TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acid:
                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 8.
TELECOMMUNICATION INFORMATION
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bonadio, Jeffrey
TITLE OF INVENTION: NUCLECTIDE AND PROTEIN SEQUENCES
TITLE OF INVENTION: OF LIVER ACTIVIN/INHIBIN AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 72
                                                 ASFHSAVFSLLKANNEWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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COUNTRY:
                                                                                                                                                                                                                                             TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
SOFTWARE: FastSE
                                                                                                                                                                                                                                                                                                                                                           NAME: Coruzzi, Laura A REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Pennie & Edmonds STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER:
                                                                                                                                                                                                       350 AA; 38517 MW; 615058 CN;
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STANDARD;
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                                                                                                                                                    Score 913; DB 13; 1
Pred. No. 1.07e-103;
1; Mismatches 0;
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PRT;
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251 AA
                                                                                                                                                                             Length 350;
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Matches 116; Conservation
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US-08-752-919-4
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                                                                                                     Sequence 4, Application US/08752919
                                                                                                                                                XXXXXX
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GENERAL INFORMATION:
APPLICANT: Bonadio, Jeffrey
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
TITLE OF INVENTION: OF LIVER ACTIVIN/INHIBIN AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                             Sequence 4, Application US/08752919
GENERAL INFORMATION:
APPLICANT: Bonadio, Jeffrey
TITLE OF INVENTION: NUCLEOTIDE;
TITLE OF INVENTION: OF LIVER AC'
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                         133 RARRETPTCEPETPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 192
                                                                                                                                                                                                                      193 ASFHSAVFSLLKANNPWPAGSSCCVPTARRPLSLLYLDHNGNVVKTDVPDMYVEACGCS 251
                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:

NAME: COTUZZI, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8464
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                             61 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 119
                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 251 AA; 28019 MW; 316319 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCTWARE: FastSEO Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
          CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 11-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 20-NOV CLASSIFICATION: 42/
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                                                                                                                                                                                                                                                                                                                                                             amino acid
)GY: linear
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 3: Pennie & Edmonds
1155 Avenue of the Americas
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                                                                                                                                                                     STANDARD;
                              NUCLEOTIDE AND PROTEIN SEQUENCES OF LIVER ACTIVIN/INHIBIN AND METHODS BASED THEREON 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/752,919
                                                                                                                                                                                                                                                                                                       Score 906; DB 13;
Pred. No. 9.23e-103;
                                                                                                                                                                                                                                                                                              Pred. No. 9.23e-
2; Mismatches
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                                                                                                                                                                     PRT;
                                                                                                                                                                     350 AA
                                                                                                                                                                                                                                                                                                                  Length 251;
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RESULT
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Best Local Similarity 97.5%;
Matches 116; Conservative
Query Match 89.3%;
Best Local Similarity 100.0%;
Matches 105; Conservative
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                                                       SEQUENCE
                                                                                  GENERAL INFORMATION:

APPLICANT: BORBZZI, VIVIEN
APPLICANT: BORBZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOO0127
CURRENT APPLICATION NUMBER: US/60/162,247
CURRENT FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 5442
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4023
LENGTH: 112
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                  US-60-162-247-4023
                                                                                                                                                                                                                                                                                                         Sequence 4023, Application US/60162247
                                                                                                                                                                                                                                                                              Sequence 4023, Application US/60162247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232 RARRRTPTCEPETPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ASFHSAVESLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RARRRIPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 60
                                                        ORGANISM: Human
QUENCE 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 1110-
MOLECULE TYPE: protein
MOLECULE TYPE: protein
MOLECULE TYPE: protein
MOLECULE TYPE: 619834 CN;
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LENGTH: 350 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 84
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASFHSAVFSLLKANNPWPAGSSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 20-NOV-1996 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM CONTROL OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Coruzzi, Laura REGISTRATION NUMBER:
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                                                            12324 MW; 66422 CN;
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Pred. No. 9.23e-103;
2; Mismatches 1;
 Pred. No. 4.97e
0; Mismatches
                 Score 818; DB 3;
Pred. No. 4.97e-91;
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   0;
                              Length 112
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    Indels
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8 PLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIAASFHSAVFSLLKA 67

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ID US-60-163-123-1750
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Best Local
              SEQUENCE
                                                                                                                                                                                                                                               Sequence 1750, Application US/60163123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-60-169-840-7660
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                                                                  NUMBER OF SEQ ID NOS: 1986
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1750
                                                                                                                                                                                                        Sequence 1750, Application US/60163123 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Fas
SEQ ID NO 7660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7660, Application US/60169840 GENERAL INFORMATION:
                                                                                                         TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOO0137
CURRENT APPLICATION NUMBER: US/60/163,123
CURRENT FILING DATE: 1999-11-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BONAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000164
                                                                                                                                                                                                                                                                                                                                                                                    74 NNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGC 118
                                                                                                                                                                                                                                                                                                                                                                                                    68 NNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                         14 PLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIAASFHSAVFSLLKA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/60/169,840 CURRENT FILING DATE: 1999-12-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 NNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGC 118
                                                                                                                                                                                            APPLICANT: Bonazzi, Vivien
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SOFTWARE: FastSEQ for Windows Version 4.0
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                             ORGANISM: Human
                                          LENGTH: 104
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 PLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIAASFHSAVFSLLKA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 89.3%;
Local Similarity 100.0%;
es 105; Conservative
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QUENCE 112 AA; 12324 MW; 66422 CN;
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Pred. No. 4.97e-91;
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Matches
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Best Local Similarity 100.0%;
                                                                                                                                                                                          SEQUENCE
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                                                                                              232 RVRRRGIDCQGASRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGIS 291
352 S 352
                                                    292 ASFHTAVLNLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGC 351
                                                                                                                                  y Match 69.0%;
Local Similarity 63.6%;
hes 77; Conservative
                                                                                                                                                                                                                                         TELEFAX: 212-869-8864
TIELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acid
                           61 ASFHSAVFSLLKANNPW-PAS-TSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGC
                                                                               1 RARRETPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 60
                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 352 AA; 39401 MW; 617722 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/752,919
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TELEFAX: 212-869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 20-NO CLASSIFICATION: 42
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                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                        NAME: Coruzzi, Laura A REGISTRATION NUMBER: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10036/2711
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STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                               amino acids
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                                                                                                                                  Score 632; DB 13; Length 352; Pred. No. 2.10e-66; Endels 16; Indels
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2

Gaps

118

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Sequence 2, Application US/08752919

GENERAL INFORMATION:
APPLICANT: BONDAIO, Jeffrey
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
TITLE OF INVENTION: OF LIVER ACTIVIN/INHIBIN AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 CCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIAASFHSAVFSLLKANN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 PWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 119
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Search completed: Thu Aug 17 10:23:58 2000 Job time : 191 secs.

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2 916 100.0 119 4 PCT US95-0 Sequence 12, Applicati 2.84e-81 3 916 100.0 119 2 US-08-755 Sequence 12, Applicati 2.84e-81 3 916 100.0 350 4 PCT US95-0 Sequence 14, Applicati 2.84e-81 5 916 100.0 350 2 US-08-765- Sequence 14, Applicati 2.84e-81 6 629 68.7 352 1 US-08-482- Sequence 14, Applicati 2.84e-81 6 629 68.7 352 1 US-08-482- Sequence 14, Applicati 1.09e-50 8 616 67.2 352 1 US-08-482- Sequence 17, Applicati 1.09e-50 18.5 106 1 US-08-482- Sequence 24, Applicati 1.09e-50 18.5 106 1 US-08-482- Sequence 24, Applicati 1.16e-38 19.8 54.4 121 4 PCT US94-0 Sequence 27, Applicati 1.16e-38 15.4 4 121 1 US-08-481- Sequence 21, Applicati 1.16e-38 15.4 4 121 1 US-08-481- Sequence 21, Applicati 1.16e-38 15.4 4 122 1 US-08-481- Sequence 21, Applicati 1.16e-38 15.4 4 122 1 US-08-481- Sequence 21, Applicati 1.16e-38 16.4 498 54.4 122 1 US-08-485- Sequence 27, Applicati 1.16e-38 18.4 498 54.4 122 1 US-08-581- Sequence 17, Applicati 1.16e-38 18.4 498 54.4 122 2 US-08-581- Sequence 17, Applicati 1.16e-38 19.4 49.8 54.4 122 2 US-08-581- Sequence 27, Applicati 1.16e-38 19.4 49.8 54.4 122 2 US-08-581- Sequence 27, Applicati 1.16e-38 19.4 54.4 122 2 US-08-581- Sequence 27, Applicati 1.16e-38 19.4 54.4 122 2 US-08-581- Sequence 31, Applicati 1.16e-38 19.4 54.4 122 2 US-08-581- Sequence 27, Applicati 1.16e-38 19.5 54.4 122 2 US-08-581- Sequence 31, Applicati 1.16e-38 19.5 54.4 122 2 US-08-581- Sequence 31, Applicati 1.16e-38 19.5 54.4 122 2 US-08-581- Sequence 31, Applicati 1.16e-38 19.5 54.4 122 2 US-08-581- Sequence 31, Applicati 1.16e-38 19.5 54.4 122 2 US-08-581- Sequence 31, Applicati 1.16e-38 19.5 54.4 122 2 US-08-581- Sequence 31, Applicati 1.16e-38 19.5 54.4 122 2 US-08-581- Sequence 31, Applicati 1.16e-38 19.5 54.4 122 2 US-08-581- Sequence 31, Applicati 1.16e-38 19.5 54.4 122 2 US-08-581- Sequence 31, Applicati 1.16e-38 19.5 54.4 122 19.5 54.4 122 2 US-08-581- Sequence 31, Applicati 1.16e-38 19.5 54.4 122 2 US-08-581- Sequence 31, Applicati 1.16e-38 19.5 54.4 19.5 54.4 19.5 54.4 19.5 54.4 19.5 54.4 19.5 54.4 19.5 54.4 19.5	greater than or equal to the score of the result be is derived by analysis of the total score distribution SUMMARIES Query Q	Gap 11 Gap 11 earched: 145341 seqs, 14437480 residues ost-processing: Minimum Match 0% Listing first 45 summaries a-issued atabase: a-issued 1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfi tatistics: Mean 28.293; Variance 116.314; scale 0.243 Pred. No. is the number of results predicted by chance to have score of the result being	**************************************
CC OPERATING SYSTEM: DOS CC SOFTWARE: FastESQ Version 1.5 CC CURRENT APPLICATION DATA: CC APPLICATION NUMBER: PCT/US95/08745 CC FILING DATE: 12-JUL-1995 CC APPLICATION: CC ATTORNEY/ACENT INFORMATION: CC NAME: Haile, Ph.D., Lisa A CC REGISTRATION NUMBER: 38,347 CC REGISTRATION NUMBER: 07265/042WO1 (FD-3830) CC TELEPHONUE: 619-678-5070 CC TELEPHONE: 619-678-5099 CC TELEPAX: 619-678-5099 CC TELEPAX: 619-678-5099 CC SEQUENCE CHARACTERISTICS: CC SEQUENCE CHARACTERISTICS: CC SEQUENCE CHARACTERISTICS: CC TYPE: anino acids CC TYPE: anino acids CC TYPE: I19 anino acids CC TYPE: Tinear CC MOLECULE TYPE: protein CC ANTI-SENSE: NO	CC STREET: 4225 Executive Square, Suite 1400 CC CITY: La Jolla CC STATE: CA CC COUNTRY: USA CC CIP: 92037 CC CMPUTER READABLE FORM: CC MEDIUM TYPE: Diskette CC COMPUTER: IBM Compatible	Sequence 12, Application PC/TUS9508745 Sequence 12, Application PC/TUS9508745 GENERAL INFORMATION: APPLICANT: THE JOHNS HOPKINS UNIVERSITY TITLE OF INVENTION: GROWTH DIFFERENTIAN NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardson STREET: 4225 Executive Square. Suite	8 U 22222222222222222222222222222222222

1.16e-38 1.16e-38 1.16e-38 1.16e-38 1.16e-38 1.16e-38 1.17e-36 1.74e-36 4.74e-36 4.74e-36 4.74e-36 5.97e-36 1.19e-35 1.19e-35

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Best Local Similarity 100.0%;
Matches 119; Conservative
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GENERAL INFORMATION:
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APPLICATION NUMBER: PCT/US95/08745
FILING DATE: 12-JUL-1995
ATTORNEY,AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A
REGISTRATION NUMBER: 38,347
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ORIGINAL SOURCE:
                     FRAGMENT TYPE: internal ORIGINAL SOURCE: 119 AA; 13161 MW; 75307 CN;
                                                                                                                                                                                          REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
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MEDIUM TYPE: Diskett
                                                        HYPOTHETICAL: N
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                                                                                                                                            SEQUENCE CHARACTERISTICS
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                                                                                              TOPOLOGY: 11
                                                                                                                      TYPE:
                                                                                                                              LENGTH:
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SOFTWARE: FastSEQ Version 1.5
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Pred. No. 2.84e-81;
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                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                    MOLECULE TYPE:
FRAGMENT TYPE:
UENCE 119 AA; :
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskett
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STREET: LA JOLIA
CHATE: CA
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APPLICANT: Lee, Se-Jin
APPLICANT: Esquela, Aurora F.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa
                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 619-678-5070
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                                                                                                      TOPOLOGY:
                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                           FILING DATE:
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                                                                                                                                                                                                       NAME: Haile, Ph.D., Lisa A. REGISTRATION NUMBER: 38,347
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Similarity 100.0%;
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                                  Score 916; DB 2;
Pred. No. 2.84e-81;
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                       Mismatches
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                                                                                                                 292 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 350
                                                                                                                                                              232 RARRRTPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 291
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                                                                                            51
                                                                                                                                                                                  Match 100.0%; Local Similarity 100.0%; es 119; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acid
                                                                                                                                       1 RARRETPTCEPATFLCCREDHYVDFQELGWRDWILOPEGYQLNYCSGQCPPHLAGSPGIA 60
                                                                                                                                                                                                                                              FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 12-JUL-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa, A
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/042WO1 (FD-3830)
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Fish & Richardson
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
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                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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                                                                                            ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 119
                                                                                                                                                                                                                                                                                                                            TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
COMPUTER: II
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TELEFAX: 619-678-5099
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Pred. No. 2.84e-81;
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                                Sequence 4, Application US/08482577B
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GENERAL INFORMATION:
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Sequence 4, Application US/08482577B Patent No. 5807713
                                                                                                                                                                  292 ASFHSAVESLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 350
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Local Similarity 100.0%;
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                   1 RARRRTPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UNDER: PCT/
PILING DATE: 12-UUL-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Haile, Ph.D., Lisa A REGISTATION NUMBER: 38,347 REFERENCE/DOCKET NUMBER: 07: TELECOMMUNICATION INFORMATION: TELEPHONE: 619-678-5070
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ORIGINAL SOURCE:
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ANTI-SENSE:
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COMPUTER: I
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STREET: 4225 Executive Square, Suite 1400
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Pred. No. 2.84e-81;
0; Mismatches 0
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Best Local Similarity 62.8%;
Matches 76; Conservative
                                                                                              XXXXXX
                                              Sequence 11, Application US/08455550
                                                                                                                     US-08-455-550-11
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                      119 S 119
                                                                                                                                                                                                                                                                                         232 RVRRRGIDCOGGSRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGIS 291
          Sequence 11, Application US/08455550 Patent No. 5670338
                                                                                                                                                                                             352 S 352
                                                                                                                                                                                                                                  292 ASFHTAVLNLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGC 351
GENERAL INFORMATION:
                                                                                                                                                                                                                    61 ASFHSAVFSLLKANNPW-PAS-TSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: HOTTEN
                                                                                                                                                                                                                                                                  1 RARRETPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDAL STREET: SUITE ... STREET: SUITE ... CITY: WASHINGTON DC ... DC ... DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: KLESNER, SHARON
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/538-5000
                                                                                                                                                                                                                                                                                                                                                                PUBLICATION INFORMATION:
DOCUMENT NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
FELING DATE: 13-AUG-1994
JENCE 352 AA; 39387 MM; 619423 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKALDO, MARMELSTEIN, MURRAY, AND ORAM
STREET: 655 FIFTENTH STREET, N.W., G STREET LOBBY,
STREET: SUITE 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, SHARON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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linear
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                                                                                                                     STANDARD;
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Best Local 9
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                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                          Sequence 2, Application US/08482577B
        Sequence 2, Application US/08482577B Patent No. 5807713 GENERAL INFORMATION:
                                                                                                                                                                                             69 ASEHTTVLNLIKANNIQTAVNSCCVPTKRRPLSMLYFDRNNNVLKTDIADMIVEACGCS 127
                                                                                                                                                                                                                                                                             / Match 67.4%; Local Similarity 62.2%; les 74; Conservative
                                                                                                                                                                                 61 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 119
                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
                                                                                                                                                                                                                              TOPOLOGY: line
MOLECULE TYPE: p
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/5
FILING DATE: 05-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
APPLICANT:
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ADDRESSEE: Dike, Bronstein, Roberts & Cushman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MURAKAMI, KAZUO
APPLICANT: UENO, NAOTO
APPLICANT: KATO, VUKIO
TITLE OF INVENTION: XENOPUS LAEVIS BONE MORPHOGENETIC PROTEINS AND USE THE
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELLEFAX: UZ 200291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Eisenstein, Ronald I REGISTRATION NUMBER: 30628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/0 FILING DATE: 30-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 31-MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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HOTTEN, GERTRUD
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                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                           234 HRRGIDCQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAAS 293
                                                                                                                               Patent No.
                                                                                                                                 Sequence 24, Application US/08482577B Patent No. 5807713
                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 63.9%; tes 76; Conservation
                                                                GENERAL INFORMATION:
APPLICANT: HOTTEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202,638-4810
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
                                                                                                                                                                                                                                                                                                 63 FHSAVFSLLKANNPW-PAST-SCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 119
                                                                                                                                                                                                                                                                                                                                                  3 RRRTPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIAAS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY, AND ORAM STREET: 655 FIFTEENTH STREET; N.W., G STREET LOBBY, STREET: SUITE 330
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ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, SHARON
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: NIKAIDO, MARMELSTEIN, MURRAY, AND ORAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
ENCE 352 AA; 38238 MW; 599802 CN;
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BECHTOLD, ROLF
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linear
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Pred. No. 1.37e-50;
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Best Local
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                                                                                                                                                                                                                                                                       Sequence 19, Application PC/TUS9400685
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                                                                                                                                                                                                                                Sequence 19, Application PC/TUS9400685 GENERAL INFORMATION:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, SHARCN
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: 9564
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEPAX: 202/638-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 CCRRDHYVDEQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIAASPHSAVESLLKANN 75
                                                                                                                                                                                                                                                                                                                                                                                                                  63.5%;
Local Similarity 68.9%;
es 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    76 PW-PAST-SCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 119
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  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: PCT/US94/00685
FILING DATE: 12-JAN-1994
                                                                                                                                                                              APPLICANT: THE JOHNS HOPKINS UNIVERSITY
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                              STREET: 1880 Centu
CITY: Los Angeles
STATE: California
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                    COUNTRY:
                                                                                                                                                                       ADDRESSEE:
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                                                                                                         90067
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1880 Century Park East, Suite 500
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Pred. No. 3.85e-47;
21; Mismatches 10; Indels
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TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
GTPANDEPNESS: SIGNIO
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                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
           ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. Ph.D., JOHN R.
REGISTRATION NUMBER: 31,678
                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: 12-JAN-19
                                                                                                                                                                                                                          ADDRESSE: SPENSLEY HORN JUBAS & LUBITZ
                                                                                                                                                                                                                                                      APPLICANT: JOHNS HOPKINS UNIVERSITY
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Wetherell, Jr. Ph.D., John R. REGISTRATION UNMBER: 31,678
REFERENCE/DOCKET NUMBER: FD3288
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                  CLASSIFICATION:
                                                                                                                                                                                                    STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR CITY: LOS ANGELES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Protein LOCATION: 1..121
 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE: Inhibin betaA
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                                                                                                                                                                   90067
                                                                                                                                                                                          CALIFORNIA
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                                                              12-JAN-1994
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                                                                         PCT/US94/00666
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Pred. No. 1.16e-38;
Pred. No. 1.16e-38;
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 FD2279 PCT
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SEQUENCE 121 AA; 13757 MW; 76294 CN;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21, Application US/08481377
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GROWTH DIFFEREN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RARRETPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 54.4%;
Local Similarity 45.5%;
                                               CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/US94/00666
FILLING DATE: 12-CAN-1994
ANTIONEY/AGENT INFORMATION:
ANTICKNEY/AGENT INFORMATION:
                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                           TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
NAME: WETHERELL, JR. Ph.D., JOHN R. REGISTRATION NUMBER: 31,678 REFERENCE,DOCKET NUMBER: ED2279 PCT TELECOMMUNICATION INFORMATION:
                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenth Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein IMMEDIATE SOURCE: CLONE: Inhibin beta A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
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                                                                                                                     FILING DATE:
                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                 STATE: CALIFORNIA
                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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Pred. No. 1.16e-38;
32; Mismatches 32
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TELEPHONE:

(619) 455-5100

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                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY
APPLICANT: THE JOHNS HOPKINS UNIVERSITY
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (619) 455-5110 INFORMATION FOR SEQ ID NO:
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Local Similarity 45.5%;
les 55; Conservative
                                                                                SOFTWARE: Patentin Release #1.0, Ver.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,835
FILING DATE: 23-OCT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00685
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MOLECULE TYPE:
                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Wetherell, Jr. Ph.D., John R. REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD3288
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASFHSAVFS-L-LKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGC 118
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                                                         FILING DATE: 12-JAN-1994
ATTORNEY/AGENT INFORMATION:
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LOCATION: 1..121
NCE 121 AA; 13757 MW; 76294 CN;
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CITY: I
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                                                                                                                                                                                                                                               CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                    ADDRESSEE:
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1880 Century Park East, Suite 500
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linear
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Pred. No. 1.16e-38,
32; Mismatches 3;
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                                                                                                                                                              Version
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ASFHSAVES-L-LKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC 120
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APPLICANT: JOHNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RRRRRGLECDGKVUICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 11
                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FORDATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
                                ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. Ph. REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3 NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Protein
LOCATION: 1..121
RCE 121 AA; 13757 MW; 76294 CN;
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STRANDEDNESS: si
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                                                                                                                          APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                          CITY: LOS ANGELES
STATE: CALIFORNIA
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Similarity 45.5%;
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                                                                                                                                      US/09/153,733A
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Pred. No. 1.16e-38;
32; Mismatches 32
                                                                                          08/481,377
                                            31,678
                                                        Ph.D., JOHN R.
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                                  FD2279 PCT
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 121 amino acid

21:

121 amino acids

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Best Local
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SEQUENCE 121 AA; 13757 MW; 76294 CN;
     ZIP: 30067

ZIP: 90067

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,559
FILING DATE: 31-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. PH.D., JOHN R.
REGISTRATION NUMBER: 31.678
REFERENCE/DOCKET NUMBER: PD2280
TELEPHONE: 619/455-5100
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                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: LEE, SE-JIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ASFHSAVES-L-LKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LEE, SE-JIN
APPLICANT: HUYNH, THANH
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 1
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TELEFAX:
                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
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Similarity 45.5%;
55; Conservative
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619-455-5110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 498; DB 3; Lo
Pred. No. 1.16e-38;
32; Mismatches 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          122
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Best Local (
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                                                                                       61 ASFHSAVFS-L-LKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGC 118
                                                                                                              62 LSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC 121
                                                                                                                                                                                     / Match
Local Similarity 45.5%;
pes 55; Conservative
                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
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                                                                                                                                                    TOPOLOGY: lir
MOLECULE TYPE:
IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                      CLONE:
FEATURE:
                                                                                                                                      RARRETPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA
                                                                                                                                                                                                                                  NAME/KEY: Protein
LOCATION: 1..122
NCE 122 AA; 13894 MW; 77513 CN;
                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                             SOURCE:
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Pred. No. 1.16e-38;
32; Mismatches 32;
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rch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. 9 Thu Aug 17 10:16:58 2000; MasPar time 5.83 Seconds 632.596 Million cell updates/sec

Description:
Perfect Score:
Sequence: >US-08-765-662-12 (1-119) from 5929213.pep 916 1 RARRETPTCEPATPLCCRRD......NGNYVKTDVPDMYVEACGCS 119

Title:

Scoring table: PAM 150 Gap 11

Searched: 85661 seqs, 30989116 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot38 1:swissprot

Statistics: Mean 40.432; Variance 56.147; scale 0.720

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Ž	Sult No.	Score	% Query Match	Length DB	æ	Ħ	Description	Pred. No.
:	<u></u>	906	œ	- ;	- ;	IHBE_MOUSE	INHIBIN BETA E CHAIN P	1.23e-229
	ν	899	98.1	350	_	1 1	BETA E CHAIN	.53e-22
	ω	632	9		_	IHBC_MOUSE	INHIBIN BETA C CHAIN P	2.46e-148
	4	616	7.		_	IHBC_HUMAN	INHIBIN BETA C CHAIN P	.21e-1
	υ	506	<u>ب</u>			IHBA_HORSE	IN BETA A CHAIN	.23e-J
	o,	503			_	IHBA_SHEEP	BETA A CHAIN	.00e-1
,	7	498			_	IHBA_MOUSE	INHIBIN BETA A CHAIN P	•
	8	498	٠		_	IHBA_RAT	INHIBIN BETA A CHAIN P	.49e-1
	ø	498			Н	IHBA_PIG	INHIBIN BETA A CHAIN P	.49e-
	10	498	54.4		_	IHBA_BOVIN	INHIBIN BETA A CHAIN P	. 496
	11	498	54.4		_	IHBA_HUMAN	BETA A CHAIN	2.49e-109
	12	477			-	IHBA_CHICK	BETA A	2.75e-103
	13	474	51.7		~	IHBB_CHICK	INHIBIN BETA B CHAIN P	.00e-
	14	471	۲		_	IHBB_MOUSE	B CHAIN	.45e-
	15	468			-	IHBB_PIG	INHIBIN BETA B CHAIN P	
	16	468			μ	IHBB_HUMAN	BETA B CHAIN	.05e-
	17	468	۲		سم	IHBB_BOVIN	INHIBIN BETA B CHAIN P	.05e-
	18	359	39.2		_	DVR1_BRARE	DVR-1 PROTEIN PRECURSO	.68e-
	19	355	œ		μ	BMPA_XENLA	BONE MORPHOGENETIC PRO	.00e-
	20	355	8		;_	BMPB_XENLA	BONE MORPHOGENETIC PRO	.00e-6
	21	352	8		μ	BMP4_XENLA	BONE MORPHOGENETIC PRO	6.84e-68
	22	352	œ		۲	BMP4_MOUSE	BONE MORPHOGENETIC PRO	· m
	23	352	38.4		-	BMP4_HUMAN	BONE MORPHOGENETIC PRO	6.84e-68

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
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34.9	35.0	35.3	35.4	35.4	35.6	35.7	35.7	36.1	36.1	37.1	37.2	37.8	38.2	38.2	38.2	38.2	38.2	38.2	38.3	38.4	38.4
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BONE MORPHOGENETIC PRO	BONE MORPHOGENETIC PRO	DECAPENTAPLEGIC PROTEI	DECAPENTAPLEGIC PROTEI	EMBRYONIC GROWTH/DIFFE	DECAPENTAPLEGIC PROTEI	BONE MORPHOGENETIC PRO	BONE MORPHOGENETIC PRO	BONE MORPHOGENETIC PRO	DVR-1 PROTEIN PRECURSO	UNIVIN PRECURSOR.	EMBRYONIC GROWTH/DIFFE	BONE MORPHOGENETIC PRO									
. 83e-	2.57e-59	7.24e-60	.84e-	3.84e-60	.08e-	5.73e-61	5.73e-61	4.52e-62	4.52e-62	1.47e-64	7.75e-65	3.18e-66	2.46e-67	2.46e-67		2.46e-67	2.46e-67	2.46e-67	.30e	6.84e-68	6.84e-68

ALIGNMENTS

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between the SWISS INSTITUTE OF BIOINFORMATICS and the EMBL OUTSTALLOR the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). EMBL: U96386; AAB53801.1; MGD; MGI:109269; INHBE. PFAM; PF00019; TGF-beta; 1. PRINTS; PR001438; GFCYSKNOT.	ERYTHROPOJESIS, STIMULATE INSULIN SECRETION, AND PROMOTE NEURAL CELL SURVIVAL. ACTIVINS ARE ALSO IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT. -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.		SEQUENCE FROM N.A. TISSUE-LIVER; MEDLINE; 97096313. MEDLINE; 97096319. Fang J., Yin W., Smiley E., Wang S.Q., Bonadio J.; "Molecular cloning of the mouse activin beta E subunit gene."; Biochem. Biophys. Res. Commun. 228:669-674(1996).	15-JUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 15-JUL-1999 (Rel. 38, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 15-JUL-1999 (Rel. 38, Last sequence update) 15-JUL-1999 (Rel. 38, Last sequence update) 11-11-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 15-JUL-1999 (Rel. 38, Last	IT 1 HBE_MOUSE STANDARD; PRT; 350 AA.

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RESULT IN ACCORDANCE OF THE PROPERTY OF THE PR
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O'Bryan M.K., Sebire K., Hedger M.P., Hearn M.T.W., de Kretser D.M.;
"The cloning and regulation of the rat activin be subunit.";
Submitted (Sep-1998) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: INHIBINS ARE GONADAL GLYCOPEPTIDES THAT INHIBIT THE
SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
ACTIVINS ACTIVATE THE SECRETION OF FOLLITROPIN. ACTIVINS REGULATE
GROWTH AND DIFFERENTIATION OF EMBRYONAL CARCINOMA CELLS, INDUCE
ERYTHROPOIESIS, STIMULATE INSULIN SECRETION, AND PROMOTE NEURAL
CELL SURVIVAL. ACTIVINS ARE ALSO IMPORTANT IN FMEROVONIC NEURAL
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088959;
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                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                     PRINTS; PR00438; GFCYSKNOT PROSITE; PS00250; TGF_BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
INHIBIN BETA E CHAIN PRECURSOR (ACTIVIN BETA-E CHAIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEVELOPMENT.
SUBURIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS (BY SIMILARITY).
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RARRRIPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 60
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                                                                                                                                                                                                                                                    PF00019; TGF-beta;
                                                                                                                                                                                                                                                                          AF089825; AAC36741.1; -.
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                               Fang J., Wang S.Q., Smiley E., Bonadio J.;

"Genes coding for mouse activin beta C and beta E are closely linked and exhibit a liver-specific expression pattern in adult tissues.";

Biochem. Biophys. Res. Commun. 231:655-661(1997).

-!- FUNCTION: INHIBINS ARE GONADAL GLYCOPEPTIDES THAT INHIBIT THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND ACTIVINS ACTIVANTE THE SECRETION OF FOLLITROPIN. ACTIVINS REGULATE GROWTH AND DIFFERENTIATION OF EMBRYONAL CARCINOMA CELLS, INDUCE EXCITATION OF EMBRYONAL CARCINOMA CELLS.
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EMBL; X90841; CAA62347.1;
EMBL; X90842; CAA62347.1;
EMBL; X90819; CAA62333.1;
                                                                              use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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Mammalia; Eutheria;
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                                                                                                                                                                                          between
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"Structural analysis of the mouse ac
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                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through a collable ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                          DEVELOPMENT.
SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DIS TISSUE SPECIFICITY: MAINLY EXPRESSED IN THE SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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Metazoa; Chordata; C
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Sciurognathi; Muridae
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Follitropin
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                                                             BIOCHEM. BLOPHYS. Res. COMMUN. 206:608-613(1995).

-!- FUNCTION: INHIBINS ARE GONADAL GLYCOPEPTIDES THAT INHIBIT THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND ACTIVINS ACTIVATE THE SECRETION OF FOLLITROPIN. ACTIVINS REGULATE GROWTH AND DIFFERENTIATION OF EMBRYONAL CARCINOMA CELLS, INDUCE ERYTHROPOIESIS, STIMULATE INSULIN SECRETION, AND PROMOTE NEURAL CELL SURVIVAL. ACTIVINS ARE ALSO IMPORTANT IN EMBRYONIC AXIAL
                                                                                                                                       Hoetten G., Neidhardt H., "Cloning of a new member activin beta C chain.";
                                                                                                                                                                                                         INHBC.
Homo sapiens (Human).
Homo sapiens (Human).
Chordata;
Metazoa; Chordata;
Primates;
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                                SUBUNIT: DIMERIC, SIMILARITY: BELOW
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                                 TGF-BETA FAMILY.
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No. 2.46e-148;
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PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR00672; INHIBINBC.
PROSITE: PS00250; TGF_BETA_1
F011iropin inhibitor; Contr
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
1NHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN)
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HSSP; P18075;
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                                                                                                                                                                                                           Equus caballus (Horse).
Eukaryota; Metazoa; Cho
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                                                                                                                                    K., Matsuyama S., Nishiha
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itor; Contraceptive;
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Pred. No. 1.2
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01-NOV-1995 (Rel. 32, I
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INHIBIN BETA A CHAIN PF
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                                                                                                                                                                                                                                                                                                 Fleming J.S., Galloway
Greenwood P.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ovis aries (Sheep).
           MOÎ. REPIOD. DEV. 40:1-8(1995).

-!- FUNCTION: INHIBLN IS A GONADAL GLYCOPEPTIDE THAT INHISECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON 1 ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT:
-!- SUBBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BOY INHIBLN A IS A DIMER OF ALPHA AND BETA-B.
INHIBLN A IS A DIMER OF ALPHA AND BETA-B.
ACTIVIN AB IS A DIMER OF BETA-A.
ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                       MEDLINE; 95217464.
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Q1-NOV-1997
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    + +
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"Activins are expressed in preimplantation mouse embryos and EC cells and are regulated on their differentiation." Development 117:711-723(1993).
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 93321614.
Albano P.M., Groome N.,
                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
HSSP;
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                INHIBIN IS A GONADAL GLYCOPEPTIDE THAT INHISCRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON TACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVINFORTANT IN EMBRYONIC AXIAL DEVELOPMENT.

1. SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BON INHIBIN A IS A DIMER OF ALPHA AND BETA-A.

INHIBIN B IS A DIMER OF ALPHA AND BETA-B.

ACTIVIN A IS A DIMER OF BETA-A.

ACTIVIN A IS A DIMER OF BETA-A AND BETA-B.

1. TISSUE SPECIFICITY: UTERUS, OVARY, AND LIVER.
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PFAM; PF00688; TGFb_propeptide;
PRINTS; PR00438; GETYSKNOT.
PRINTS; PR00670; INHIBINBA.
PROSITE; PS00250; TGF_BETA_1; 1
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56; Conser
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1 27 POTENTIAL.
28 309 POTENTIAL.
310 425 INHIBIN BE
310 321 BY SIMILAR
320 390 BY SIMILAR
320 BY SIMILAR
349 422 BY SIMILAR
349 422 BY SIMILAR
353 424 BY SIMILAR
369 389 INTECIAIN
365 165 POTENTIAL
  SPECIFICITY: UTERUS, OVARY, AND LIV
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(Rel. 28, Last sequence update)
(Rel. 35, Last annotation update)
A CHAIN PRECURSOR (ACTIVIN BETA-A
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INTERCHAIN (BY SIMILARITY).
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31;
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                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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No. 9.00e-111;
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                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 91042598.
Woodruff T.K., Meunier H., Jones P.B.C., Hsueh A.J.W., Mandourier T.K., Meunier H., Jones P.B.C., Hsueh A.J.W., Mandourier T.K., Meunier H., Jones P.B.C., Hsueh A.J.W., Mandourier T.K., Meunier Hallen, Molecular cloning of alpha- and beta-subunicomplementary deoxyribonucleic acids and expression in the Molecular Endocrinol 1:561-568(1987).
                                                                                                                                                                                                                                                                                                                           IHBA_RAT
P18331;
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PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00019; TGF-beta; 1.
PFAM; PF00688; TGFb_propeptide;
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR00670; INHIBINBA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                  01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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PIR; S31440; S31440.
                                                                                                                                                                                                               Mammalia;
                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
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les 55; Conse
EUNCTION: INHIBIN IS A GONADAL GLYCOPEPTIDE THAT INHIBITS THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALS IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS. INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
INHIBIN A IS A DIMER OF ALPHA AND BETA-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #GI:96570; INF
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pin inhibitor; Contracep
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INTERCHAIN (BY SIMILARITY).
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Pred. No. 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80C251B8754A7213 CRC64;
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2.49e-109;
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the ovary.";
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IS ALSO
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23-OCT-1986
23-OCT-1986
15-JUL-1998
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DISULFID
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CARBOHYD
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                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=FOLLICULAR FLUID;
MEDLINE; 86092207.
Mason A.J., Hayflick J.S.,
                                                                                                                                                              Mason A.J., Hayflick J.S., Ling N., Esch F., Ueno N., Ying S.-Y., Guillemin R., Niall H., Seeburg P.H.; "Complementary DNA sequences of ovarian follicular fluid inhibin show
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0438; GFCYSKNOT.
PRINTS; PR00670; INHIBINBA.
PROSITE; PS00250; TGF_BETA_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00019; TGF-beta; 1.
PFAM; PF00688; TGFb_propeptide;
PRINTS; PR00438; GFCYSKNOT.
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  TISSUE=FOLLICULAR FLUID;
MEDLINE; 92355604.
                                                                                           Nature
                                                                                                                           precursor structure and homology with transforming
factor-beta.":
                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                           23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                            SEQUENCE OF 309-323
                                                                                                                      factor-beta.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ASFHSAVFS-L-LKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s 119
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                                                                                           318:659-663(1985).
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larity 45.5%;
Conservative
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INTERCHAIN (BY SIMILARITY).
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Pred. No. 2.49e-109;
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                                                                                                                                                              IHBA_BOVIN
P07995;
01-AUG-1988
01-OCT-1996
01-OCT-1996
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PFAM; PF00019; TGF-beta; 1.
PFAM; PF00688; TGFb_propeptide;
PRINTS; PR00438; GFCYSKNOT.
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SEQUENCE
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Follitropin inhibitor.
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Ariizumi T.,
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                          Bovidae;
                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                               Bos taurus (Bovine).
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SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
INHIBIN A IS A DIMER OF ALPHA AND BETA-B.
INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
ACTIVIN A IS A DIMER OF BETA-A.
ACTIVIN A IS A DIMER OF BETA-A AND BETA-B.
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: INHIBIN IS A GONADAL GLYCOPEPTIDE THAT INHIBITS THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER ACTIVIN ACTIVIN ESCRETION OF FOLLITROPIN. ACTIVIN IS ALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASFHSAVFS-L-LKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGC
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Similarity 45.5%;
55; Conservative
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                             Bovinae;
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PRECURSOR (ACTIVIN BETA-
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INTERCHAIN (BY SIMILARITY).
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436BC62226FDAF52 CRC64;
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                                                     Bovoidea
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C. PROCTION INHIBITS A DIMER OF AND BY THE PITUITARY GLAND. ON THE OTHER SECRETION OF FOLLITROPIN. ACTIVIN IS ALL DEVELOPMENT.

C. PROCTION ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALL DEVELOPMENT.

C. PROCTION TO EMBRYONIC ANIAL DEVELOPMENT.

C. PROCTION ACTIVATES THE SECRETION OF MORE DISULFIDE BONDS.

INHIBIN A IS A DIMER OF ALPHA AND BETA-A.

C. ROTIVIN AB IS A DIMER OF BETA-A.

C. ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.

C. SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                   Matches
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Best Local
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EMBL; U16238; AAB60627.1; JOINED.
EMBL; M13274; AAA97415.1; -.
PIR; B25732; B25732;
HSSP; P18075; 1BMP.
PFAM; PF00019; TGF-beta; 1.
PFAM; PF00088; TGFb_propeptide; 1
PFAM; PF00088; TGFb_BYDFOPPTIDE; PROPERTY GROUPS; TGF_BETA_1; 1.
PROSITE; PR00250; TGF_BETA_1; 1.
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CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROPEP
CHAIN
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footprinting.";
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                                                                                    RRRRRGLECDGKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSS
LSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGC
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32; Mismatches 32;
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P08476; Q14599;
01-AUG-1988 (Rel. 08, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
1NHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN) (ERYTHROID
                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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MUTATA M., Eto Y., Shibai H., Sakai Nurata M., Eto Y., Shibai H., Sakai Nurata M., Sakai
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Mason A.J., Niall H.D.,
"Structure of two human
Biochem. Biophys. Res. C
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berg H., Walter M., Submitted (MAY-1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 311-426 FROM N.A. TISSUE-TESTIS;
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-i - FUNCTION: INHIBIN IS A GONADAL GLYCOPEPTIDE THAT INHIB:
SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE
ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN
IMPORTANT IN EMERYONIC AXIAL DEVELOPMENT.

-i SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BOND:
INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
INHIBIN B IS A DIMER OF BETA-A.
ACTIVIN AB IS A DIMER OF BETA-A.

SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -
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M13436; AAA59168.1;
X04447; CAA28041.1;
X57578; CAA40805.1;
X57579; CCAA40805.1;
X57579; CAA40806.1;
J03634; AAA35787.1;
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ovarian inhibins.";
Commun. 135:957-964(1986)
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activin beta
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P27092; Q90697;
O1-AUG-1992 (Rel. 2
O1-NOV-1995 (Rel. 3
15-DEC-1998 (Rel. 3
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PIR; B24248; B24248.

PIR; B23556; B23556;

PIR; S30488; S30488.

HSSP; P18075; 1BMP.

MIM; 147290; -.
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PIR; 1
PIR; 1
PIR; 1
                                                                                 "Molecular cloning of inhibin/activin beta A-subunit complementary deoxyribonucleic acid and expression of inhibin/activin alpha- and beta A-subunits in the domestic hen."; Biol. Reprod. 54:429-435(1996).
                                                                                                                                                                    Chen
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Follitropin
TISSUE=HYPOBLAST;
MEDLINE; 91029482
                                                                                                                                                                                                         STRAIN-WHITE LEGHORN;
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INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
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                                                                                                                                                                                   MEDLINE; 96380183.
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X72498; CAA51163.1;
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PR00670; INHIBINBA.
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llarity 45.5%;
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Pred. No. 2.49e-109;
32; Mismatches 32;
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; Galliformes; Phasianidae; Phasianinae;
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EMBL: U42377; AAC59738.1; -.
EMBL: M61167; AAA48569.1; -.
EMBL: M57407; AAA03080.1; -.
PIR: B36193; B36193.
HSSP; P18075; 1BMP.
PFAM: PF00088; TGF-beta; 1.
PFAM: PF00688; TGFb_propeptide; 1
PRINTS; PR00438; GFCYSKNOT.
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expressed in the hypoblast
Cell 63:495-501(1990)
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IHBB_CHICK P27093; 073796;
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PRINTS: PRO0670; INHIBINBA.
PROSITE: PS00250; TGF_BETA_1; FALSE_NEG.
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- FUNCTION: INHIBIN IS A GONADAL GLYCOPEPTIDE THAT INH:
- SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON 'A
ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN ACTIVIN THE SECRETION OF FOLLITROPIN. ACTIVIN GENERAL DEVELOPMENT:
- INFORTANT IN EMBRYONIC AXIAL DEVELOPMENT:
- INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
INHIBIN A IS A DIMER OF ALPHA AND BETA-B.
ACTIVIN A IS A DIMER OF BETA-A AND BETA-B.
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                                                                                                                            ASFHSAVFS-L-LKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGC
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                                                                                               424
                                                                                                                                                                                                                                        Similarity 53; Conse
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larity 43.8%;
Conservative
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BY SIMILARITY.
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Pred. No. 2.
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                 391
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                                                                                                                                                                                                                                                    DB 1; I
.75e-103;
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                                                                                                                                                                                                                                                                                        PFAM; PF00688; TGFb_propeptide; PRINTS; PR00438; GFCYSKNOT. PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Activin can induce the formatio in the hypoblast of the chick."; Cell 63:495-501(1990).
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01-NOV-1997 (Rel. 35, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN).
                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                     PROPEP
                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                         Follitropin inhibitor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitrani E., Ziv T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hecht D.J., Davis A.J
Submitted (MAR-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 311-381 FROM N.A. MEDLINE; 91029482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-WHITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klinger H., Halaschek-Wiener
Submitted (JUL-1996) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-FOLLICLE
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                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
INHIBIN A IS A DIMER OF ALPHA AND BETA-B.
INHIBIN B IS A DIMER OF BETA-A.
ACTIVIN A IS A DIMER OF BETA-A.
ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: INHIBIN IS A GONADAL GLYCOPEPTIDE THAT INHIBITS SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OR ACTIVIN ACTIVIN THE SECRETION OF FOLLITROPIN. ACTIVIN IS
                                                                                                                                                                                                                                                                                                                                                              M61166; AAA48568.1; -. M57408; AAA03079.1; -. P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                 PF00019; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Z71594; CAA96248.1;
                                                                                                                                                                                                                                                                                                                                                                                                                    AF055478; AAC14187.1; -.
 Similarity 59; Conse
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Davis A.J., Ryan I.M., Johnson P.A.;
AR-1998) to the EMBL/GenBank/DDBJ databases
   Conservative
                                                                         AA;
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276
288
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                  51.7%;
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                                                                                                                                                                                                                                                                       Contraceptive; Hormone;
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                                                                         Œ;
Score 474; DB 1; L
Pred. No. 2.00e-102;
24; Mismatches 36;
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                                                                       -> PG (IN REF. 2).
060017BF33F7AF6C CRC64;
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                                   Length 391
                                                                                                                                                                                                                                                                         Glycoprotein; Signal.
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O4999; Q61277;

T 01-FEB-1994 (Rel. 28, Created)

T 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

TNUTRIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHI
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                                                                                                                                                                                                                                                                                                                                                                        HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and EC cells and are regulated on their differentiation.";
Development 117:711-723(1993).

-!- FUNCTION: INHIBIN IS A GONADAL GLYCOPEPTIDE THAT INHIBITS THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.

-!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
INHIBIN A IS A DIMER OF ALPHA AND BETA-B.
INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
ACTIVIN AB IS A DIMER OF BETA-A.
ACTIVIN AB IS A DIMER OF BETA-A. AND BETA-B.
ACTIVIN AB IS A DIMER OF BETA-A. AND BETA-B.
CJ7 EMBRYONIC STEM CELLS, AND POSSIBLY IN LIVER.

-!- TISSUE SPECIFICITY: UTERUS TESTIS, OVARY, LUNG, KIDNEY, BRAIN, CJ7 EMBRYONIC STEM CELLS, AND POSSIBLY IN LIVER.
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X83376; CAA58290.1; EMBL; X69620; CAA49326.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Albano P.M., Groome N., Smith J.C.;
Albano P.M., Groome N., Smith J.C.;
"Activins are expressed in preimplantation mouse embryos and "Activins are expressed in their differentiation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
  SEQUENCE
                                                                                                                                                                                                                  PROPEP
                                                                                                                                                                                                                                              NON_TER
                                                                                                                                                                                                                                                                  Follitropin
                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                            PFAM;
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Ritvos O., Tuuri T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CBA X NMR1; TISSUE-TESTIS;
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TE; PS00250; TGF_BETA_1; 1.
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Sciurognathi; Muridae;
2524B21DC648D9A9 CRC64;
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Matches 5
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1. Biol. Chem. 267.16385-16399(1992).

1. FUNCTION: INHIBIN IS A GONADAL GIVCOPEPTIDE THAT INHIBITS THE SECRETION OF FOLLITROPIN ACTIVIN IS J. SUGINIC AXIAL DEVELOPMENT.

1. SUGUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS. INHIBIN A IS A DIMER OF ALPHA AND BETA-A. INHIBIN B IS A DIMER OF ALPHA AND BETA-B.

2. CITVIN AB IS A DIMER OF BETA-A AND BETA-B.

3. CITVIN AB IS A DIMER OF BETA-A AND BETA-B.

4. CITVIN AB IS A DIMER OF BETA-A AND BETA-B.

3. CITVIN AB IS A DIMER OF BETA-A AND BETA-B.
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01-NOV-1986
01-NOV-1986
15-JUL-1998
                                                                                                                                        PFAM; PF00019; TGF-beta; 1.
PFAM; PF00688; TGFb_propeptide;
PFAM; PF00688; TGFB_BETA_1; 1
                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                         EMBL; X03267; CAA2702
PIR; A01394; WFPGBB.
HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mason A.J., Hayflick J.S., Ling N., Esch F., Ueno N., Ying Guillemin R., Niall H., Seeburg P.H.; "Complementary DNA sequences of ovarian follicular fluid precursor structure and homology with transforming growth
                                                                                                                                Follitropin inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE;
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Similarity 48.3%;
58; Conservative
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238
245
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(Rel. 03, Last sequence update)
(Rel. 36, Last annotation update)
A B CHAIN PRECURSOR (ACTIVIN BETA-B
                                                                                                                                                                                                                                                                                 CAA27021.1;
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349
246
314
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                                                                                                                                Contraceptive;
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27; Mismatc
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                                                                                                                              Hormone;
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Search completed: Thu Aug 17 10:17:28 2000 Time : 30 secs.

(MT)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

rch_pp protein - protein database search, using Smith-Waterman algorithm Thu Aug 17 10:17:46 2000; MasPar time 13.47 Seconds 612.688 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: Sequence: >US-08-765-662-12 (1-119) from 5929213.pep 916 1 RARRRTPTCEPATPLCCRRD.....NGNVVKTDVPDMVVEACGCS 119

Scoring table: PAM 150 Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb112

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_bhage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 39.398; Variance 61.413; scale 0.642

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 3 3 4 4 4 4 7 7 6 6 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
630 6472 4674 6723 387 387 387 352 352 352 352 352	Score
68.8 51.7 50.7 50.7 44.0 45.3 39.5 39.5 39.5 38.4 48.3 39.5 39.5 38.4 48.3 38.4	Query Match 1
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ACTIVIN BETA C. ACTIVIN D PRECURSOR. ACTIVIN BETA B SUBUNIT ACTIVIN BETA B SUBUNIT ACTIVIN BETA B. ACTIVIN BETA-B SUBUNIT ACTIVIN BETA-B SUBUNIT ACTIVIN BETA-B-2 SUBUN ACTIVIN BETA-B-1 SUBUNIT ACTIVIN BETA-B-1	Description
8.97e-132 6.7e-91 8.69e-91 9.74e-89 9.74e-89 9.34e-76 1.04e-71 3.44e-71 3.44e-69 6.14e-69 6.14e-69 6.12e-63 1.12e-61 1.11e-61 1.11e-60 1.96e-60 1.96e-60	Pred. No.

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ALIGNMENTS

RESULT ID C AC C DT C	Qy Db	Фр	Ор	Qu Be	RESULT DISCRETE RANGE OF STREET
LT 2 091696 PRELIMINARY; PRT; 367 AA. 091696; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)	351 S 351 119 S 119	291 ASFHTAPINILKANTDAGTARRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGC 350 : :	231 RVRRRGINCQGLSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCTGQCPLHVAGMPGIS 290 : : : : : : :	Query Match 68.8%; Score 630; DB 11; Length 351; Best Local Similarity 63.6%; Pred. No. 8.97e-132; Matches 77; Conservative 26; Mismatches 16; Indels 2; Gaps 2;	OPWUKS: OPWUKS: OPWUKS: OPWUKS: O1-NOV-1999 (TYEMBLITEL 12, Created) O1-NOV-1999 (TYEMBLITEL 12, Last sequence update) O1-NOV-1999 (TYEMBLITEL 12, Last annotation update) O1-NOV-1999 (TYEMBLITEL 12, Last annotation update) ACTIVIN BETA C. RATIUS NOTYPEGICUS (RAT). EUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; EUHERIA; RODENTIA; SCIULTE-HERWANN R.; EULENEE FROM N.A. STRAIN-WISTAR; "ROSSMANITH W., PETER B., SCHULTE-HERWANN R.; "ROSSMANITH W., PETER B., PETER B

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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
ACTIVIN BETA B SUBUNIT:
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                   Glycoprotein.
370
                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00250; TGF_BETA; 1.
PFAM; PF00019; TGF-beta; 1.
PFAM; PF00688; TGFb_propeptide;
PRINTS; PR00438; GFCYSKNOT.
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MEDLINE: 93773083
DOHRMANN C.E. THE MANATI-BRIVANLOU
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Q91350;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00250; TGF_BETA; PFAM; PF00019; TGF-beta; 1. PRINTS; PR00438; GFCYSKNOT.
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251 RIRKRGLECDGHTNLCCRQQFYIDFRLIGWNDWIIAPAGYYGNYCEGSCPAYLAGVPGSA 310
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Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Xenopus laevis (African clawed
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                                                                                                                                              Similarity 58; Conser
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larity 48.3%;
Conservative
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Pred. No. 2.67e-91;
25; Mismatches 36;
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Pred. No. 6.80e-129;
25; Mismatches 20;
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Xenopodinae;
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RESULT

ID Q98860;
AC Q98860;
AC Q98860;
DT 01-FEB-1997 (TIEMBLIFE1. 02, C;
DT 01-FEB-1997 (TIEMBLIFE1. 12, L;
DT 01-NOV-1999 (TIEMBLIFE1. 12, L;
DT 01-NOV-1999 (TIEMBLIFE1. 12, L;
DT 01-NOV-1999 (TIEMBLIFE). 12, L;
DT 01-NOV-1999 (TIEMBLIFE).
OC ENERTYOTA, Metazoa, Chordata;
OC ENERTYOTA, Metazoa, Chordata;
OC BATTACHIA; CAUDATA; Salamandro
RN [1]
RP SEQUENCE FROM N.A.
TISSUE-TESTIS;
RX MEDLINE; 96295508.
RR MEDLINE; 96295508.
RR MEDLINE; 96295508.
RR MEDLINE; 96295508.
RR YAMANOTO T., NAKAYANA Y., ABE
RR YAMANOTO T., NAKAYANA
RR YAMANOTO T., NAKAYANA Y., ABE
RR YAMAYANA Y
    AC RRANGOCC OCC RRANGOCC RRANGOCC RRANGOCC CCC
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Best Local
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Q90261;
01-NOV-1996
01-NOV-1996
01-NOV-1999
                    SEQUENCE FROM N.A.
MEDLINE: 95011555.
WITTBRODT J., FREDERIC R.M.;
"Disruption of mesoderm and axis
expression of activin variants: t
Genes Dev. 8:1448-1462(1994).
                                                                                                                                                                        Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neopterygii; Teleostei; Buteleostei; Ostariophysi; C
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                  ZACTBB OR ZACTBETAB
                                                                                                                                                                                                                                                                                         ACTIVIN BETA
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PFAM; PF00019; TGF-beta; 1.
PFAM; PF00688; TGFb_propeptide;
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR00670; INHIBINBA.
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Chordata; Craniata; Vertebrata.
Salamandroidea; Salamandridae;
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FACTORS
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HSSP; P18075; 1BMP.
ZFIN; ZDB-GEME-990415-2; Zactbb.
PROSITE; PS00250; TGF_BETA; 1.
PFAM; PF00608; TGF-beta; 1.
PFAM; PF00688; TGFb_propeptide; 1.
PRINTS; PR00438; GFCYSKNOT.
Glycoprotein.
09W6T8;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
ACTIVIN BETA A PROTEIN (FRAGMENT).
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SEQUENCE
                                                                                                                                                                  Q9W6T8
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Buteleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation updat
ACTIVIN BETA B PROTEIN (FRAGMENT)
ACTIVIN BETA B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9W6T9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyprinoidea; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOLDER N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RODAWAY A., TAKEDA H., KOSHIDA S., PRICE B.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           333
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                                                                                                                                                                                                                                                                                                                    81
                                                                                                                                                                                                                                                                                                                                                         Match 47.9%;
Local Similarity 49.1%;
les 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60
                                                                                                                                                                                                                                                                    88
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mes 58; Conser
                                                                                                                                                                                                                                                                    FSLLKANNPWPAST-SCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGC 118
                                                                                                                                                                                                                                                                                                          VNQYRMRGMSPGSVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1
138
138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393 AA; 43830 MW; 14DE189C CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.7%;
larity 47.9%;
Conservative
                                                                                                                                                                     PRELIMINARY;
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138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15263 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 439; DB 13;
Pred. No. 2.36e-82;
22; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 464; DB 13;
Pred. No. 9.74e-89;
24; Mismatches 37
                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9055EB6D CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMITH J.C., PATIENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 393;
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TRESULT PROCESSION OF PROCESSI
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Best Local
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Best Local
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NON_TER
SEQUENCE
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042125; O1-JAN-1998 (TIEMBLIEL. 05, Created)
01-JAN-1998 (TIEMBLIEL. 05, Last sequence update)
01-NOV-1999 (TIEMBLIEL. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTIVIN BETA B (FRAGMENT).

Pagrus major (Red sea bream) (Chrysophrys major).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Activin is an inducer of mesendoderm in the zebrafish germ ring."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
EMBL; AJ238980; CAB43091.1; -.
PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAKAKIDA Y., KASAHARA M., INABI
Submitted (AUG-1997) to the EM
-I-SIMILARITY: TO OTHER GROWFII
EMBL; AB006786; BAA22570.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00019; TGF-beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P18075; 1BMP.
PROSITE; PS00250; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=OVERY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTIVIN BETA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RODAWAY
                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                     10 RIRKRGLECDGSSSLCCRQQFYIDFRLIGWNDWIIAPSGYFGNYCEGNCPAYMAGVPGSA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69
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                                                                                                                                                                                                                     70 SSFHTAVVNQYRMRGMSPGSMNSCCIPTKLSTMSMLYFDDEYNIVKRDVP 119
                                                                                                                                                                                                                                                                                                  1 RARRRIPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 CDGKARVCCKRQFYVNFKDIGWNDWIIAPSGYHANYCEGDCASNVASITGNSLSFRSTVI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                           ASFHSAVFSLLKANNPWPAS-TSCCVPTARRPLSLLYLDHNGNVVKTDVP
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Similarity 41.4%;
46; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
52; Conser
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120
120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 AA;
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGF_BETA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13455 MW;
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he EMBL/GenBank/DDBJ databases.
~~~~~ FACTORS OF THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
24; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 421; DB 13; I
Pred. No. 8.86e-78;
34; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 415; DB 13;
Pred. No. 2.94e-76;
PRT;
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01-FEB-1997
01-FEB-1997
01-NOV-1999
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01-NOV-1996 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
ACTIVIN BETA-A SUBUNIT (FRAGMENT).
Carassius auratus (Goldfish).
Curassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; (Cyprinoidea; Cyprininae; Carassius.
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Q90390;
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GE W.; GALLIN W.J., STROBECK C., PETER R.E.;

GE Of GALLIN W.J., STROBECK C., PETER R.E.;

Cloning and sequencing of goldfish activin subunit of the sequencing of goldfish activin subunit of the sequence of the sequenc
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HSSP; P18075; 1BMP.
PROSITE; PS00250; TGF_BET?
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
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01-FEB-1997 (TYEMBLrel. 02, Last sequence up
01-NOV-1999 (TYEMBLRel. 12, Last annotation
ACTIVIN BETA-B SUBUNIT (FRAGMENT).
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YAMAMOTO T., NAKAYAMA Y., AI
"Expression of activin beta
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                                                                                                Local Similarity
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                                                              Score 387; DB 13;
Pred. No. 3.44e-69;
29; Mismatches 25;
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Pred. No. 1.04e-71;
21; Mismatches 29
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                                                                                                       MEDLINE: 93290666.

GE W., GALLIN W.J., STROBECK C., PETER R.E.;

"Cloning and sequencing of goldfish activin subunit of the structural conservation during vertebrate evolution. structural conservation during vertebrate evolution. Structural conservation during vertebrate evolution. Structural conservation during vertebrate evolution.
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MEDLINE; 93290666.

GE W., GALLIN W.J., STROBECK C., PETER R.E.;

GE W., GALLIN W.J., STROBECK C., PETER R.E.;

"Cloning and sequencing of goldfish activin subunit of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata;
Neopterygii; Teleostei; Euteleostei; Ost
Cyprinoidea; Cyprinidae; Cyprininae; Car
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TERMBLrel. 01, Created)
01-NOV-1996 (TERMBLrel. 01, Last seq)
01-NOV-1999 (TERMBLrel. 12, Last ann
ACTIVIN BETA-B-1 SUBUNIT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ol-NOV-1999 (TIEMBLIEL 12, Last annotation update)
ACTIVIN BETA-B-2 SUBUNIT (FRAMENT).
Carassius auratus (Golddish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
                                        Biochem. Biophys. Res. Commun. 1

-: SIMILARITY: TO OTHER GROWTH

EMBL; L15340; AAA49160.1; -.

HSSP; P10600; 1TGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neopterygii;
Cyprinoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 GMSPGSVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNM 102
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SIMILARITY: TO U....;

L15341; AAA49161.1; -.

P; P18075; 1BMP.

P; P18075; 1BMP.

P; P500250; TGF_BETA; 1.
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50; Conser
    PS00250;
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102 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.1%;
ilarity 51.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Cyprinidae; Cyprininae;
TGF_BETA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102
11342 MW;
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19;
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Pred. No. 6.14e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vertebrata; Actinopterygii;
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                                                                                                                                      TGF - BETA
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PANOPOULOU G.D., CLARK M.D., HOLLAND L.Z., LEHRACH H., HO!
PANOPOULOU G.D., CLARK M.D., HOLLAND L.Z., LEHRACH H., HO!
PANOPOULOU G.D., CLARK M.D., HOLLAND L.Z., LEHRACH H., HO!
PANOPOULOU G.D., CLARK M.D., HOLLAND L.Z., HOLLAND L.Z., HOLLAND L.Z., LEHRACH M.D., HOLLAND L.Z., LEHRACH M.D., HOLLAND L.Z., LEHRACH H., HO!
PANOPOULOU G.D., HOLLAND L.Z., LEHRACH H., HOLLAND L.Z., LEHRACH H., HO!
PANOPOULOU G.D., HOLLAND L.Z., LEHRA
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002424;
002424;
01-JUL-1997
01-NOV-1998
01-NOV-1999
      STRAIN-N2;
YANDELL M
                                                                                                                                                                                                                                                            01-UUL-1997 (TrEMBLrel. 04, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DECAPENTAPLEGIC PROTEIN HOMOLOG.
                                                                    SEQUENCE FROM N.A.
                                                                                                                                     Rhabditina;
                                                                                                                                                                   Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                              Caenorhabditis elegans.
                                                                                                                                                                                                                                       DBL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Branchiostoma floridae (Florida lancelet) (Amphioxus).
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOY-1999 (TrEMBLrel. 12, Last annotation updat
BONE MORPHOGENETIC PROTEIN 2/4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Branchiostoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 PLAVPKACCVPTDLSPISMLYLNENDQVVLKNYQDMVVEGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 CRRHSLYVDFSDVGWNDWIVAPPGYQAYYCHGECPFPLAD-H-LNSTNHAIVQTLVNSVN 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ycoprotein.
HOUENCE 361 AA; 41517 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 41.7%;
Local Similarity 47.6%;
les 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match
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Local Similarity 50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGC 118
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          M.D.,
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102 AA;
                                                                                                                                     Rhabditoidea;
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   R.M.,
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11358 MW;
   SUZUKI
                                                                                                                                 Rhabditidae;
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Pred. No. 6.21e-68;
20; Mismatches 31
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Pred. No. 1.09e-68;
20; Mismatches 28
                                                                                                                                 Secernentea; Rhabditia; Rhabditida;
oditidae; Peloderinae; Caenorhabditi
                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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Υ.,
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   GOOM
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W.B.;
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Best Local Similarity 41.2%;
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       MORITA K., CHOW K.L., UENO N.;

"Body Length and Male Tail Ray Pattern Fo
Regulated by a Member of TGFb Family.";
Submitted (JUN-1998) to the EMBL/GenBank/
EMBL; AF074395; AAC26791.1; -.
HSSF; P18075; IBMP.
PFAM; PF00019; TGF-beta; 1.
PRINTS; PR00438; GFCYSKNOT.
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Best Local :
time :
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076514
076514;
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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PFAM; PF00019; TGF-beta;
PRINTS; PR00438; GFCYSKN
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                      completed: Thu
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                                                                                        AASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGC
                                                                                                                                      NATNHAIIQSLLHSLRPDEVPPPCCVPTETSPLSILYMDVDKVIVIREYADMRVESCGC 364
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Similarity 41.2%;
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Pred. No. 6.32e-63;
28; Mismatches 37
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